

**FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTA  
TGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAA**ATG**TGG  
TGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTC  
ATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGT  
GACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTT  
TTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAAC  
GTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGGAAATACTGAGTTGTTTAGGACTTTCT  
ATTGTGGCAAACCTTCAGAAAAACAACCCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACC  
TTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAA  
ATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCA  
CTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAG  
AAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAA  
TGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATT  
TCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCCTCTATGACACTGCACCTTGCCCTATT  
ACAATGAACGAACACGGCTACTTTCCAGAGATATTT**TGA**TGAAAGGATAAAATATTTCTGTAA  
TGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTATTCTTCTCTGAAATTT  
TCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATAATCAGGAAACATGAAAG  
AAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTATTAAAAACACCTATGCCT  
ATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIA  
AVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAV  
LTFGMGSLYMFVQQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDL  
EQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT YIRDFQKISLRVEANLHGLTLYDTAPC  
PINNERTRLLSRDI

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 13-33

#### **Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

#### **N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

**FIGURE 3**

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGGC  
 AGACCGTGTGAGGGGGCCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGC  
 AGGAGCCTTCCTTACACTTCGCC**ATG**AGTTTCCTCATCGACTCCAGCATCATGATTACCTCCC  
 AGATACTATTTTTTGGATTGTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGA  
 TACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTG  
 AGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAA  
 TGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGCTATTTTA  
 TTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTTATGGCTGA  
 CCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTCTCAGCCCCAAAACATGGGA  
 TCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGA CTCTCATGGCTCTTC  
 TTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTCCTCAGGAATGTGA  
 CTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGATCATAAGCA  
 AAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACAAAC  
 CATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGGAAGTGAAAATCTTA  
 CTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAG  
 CTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTA  
 ATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATA  
 TTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATT  
 ATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATTTCTTCATTCTTGTGGAA  
 TAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTACCAAGTTCTTTTATGCCATCT  
 CTAGCAGTAAGTCCCTCCAATGTCATTGTCTGCTATTAGCACAGATAATGGGCATGTACTTTG  
 TCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAATACCGCACCATAATCACTGAAG  
 TCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTGATGTGATCTTCCTGGTCAGCG  
 CTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAACAGGCACCAGAGAAGCAAATGGCAC  
 CT**TGA**ACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTAGATATAAGAGG  
 GGGGAAAAATGGAACCAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGCATTTTTT  
 CACCTTCATAGCATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAGA  
 ACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGG  
 CTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGA ACTCTGGGGC  
 AAGACATGTCTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAA  
 AGGTTATAGCTTTGCCTTGAGATTGACTCATTAAAATCAGAGACTGTAACAAAAAAAAAAAAA  
 AAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACT  
 TGTTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEIL  
GVLNSSSRYPFWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFFWK  
LGDPFPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILAL  
ERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVD  
ALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGK  
TDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNV  
IVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFL  
YLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

**FIGURE 5**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTT  
 CCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTG  
 AGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACG**ATG**GCCAGGTGCTTCAGCCTGGTGTGCTT  
 CTCACCTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCC  
 ATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTG  
 AATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAA  
 GTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGGAGATGGATT  
 GTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATT  
 TGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACT  
 AACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACA  
 CAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATA  
 CCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTG  
 ATTTGTGTCACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT  
 GAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTA  
 GTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTAT  
 GTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGATCGAAACCAAAGTAGTA  
 AAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGAAAACTGATAAAAACCCA  
 GAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAAGCTGAAGTT**TAGAT**GAGA  
 CAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGG  
 GAAATCAAAGGGGCCAAAGAACCAGAAAGAAAGTCCACCCTTGGTTCCCTAACTGGAATCAGC  
 TCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGCCCTTCTCCTTATTGTAACCTT  
 GTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCTTTCTAGCCTGGCTATGTCCTA  
 ATAATATCCCCTGGGAGAAAGGAGTTTTTGCAAAGTGCAAGGACCTAAACATCTCATCAGTA  
 TCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTGAAAGCCAAGGAGTCACT  
 GAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCAGCTCTGAAAGAGAAA  
 CACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAATGGCAGAAAAGTTT  
 AGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAATAAA  
 GAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAACACAGACAGG  
 GTCAAAGTGTCTTCTCTGAACACATTGAGTTGGAATCACTGTTTGAACACACACACTTACTT  
 TTTCTGGTCTCTACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACAAAAAT  
 AAAAATCTTATAAATTTCTATTTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACT  
 CAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTCA  
 AGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCTCAAAAAATTGCACATAGTA  
 GAACGCTATCTGGGAAGCTATTTTTTTCAGTTTGGATTTTCTAGCTTATCTACTTCCAACT  
 AATTTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCT  
 TAATTTATTATTAAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAA  
 AAGTGCCATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGC  
 AGAAATATTTGTGACAAAAAATTAAAGCATTTAGAAAACCT

**FIGURE 6**

MARCFSLVLLLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRL  
 LGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKPVSQRQFAA  
 YCYNSSDTWTNSCIPEIIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPA  
 STSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFFGAAA  
 GLGFCYVKRYVKAFPFNTKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPPEESKSPSKTTV  
 RCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

**FIGURE 7**

CGCCGCGCTCCCGCACCCGCGGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCG  
GCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCGGG  
GCGGCGGCTGCGGGCGCAGAGCGGAG**ATG**CAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGC  
TGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGC  
CCGGCCCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTG  
AGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAG  
AAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAATG  
AGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGA  
TAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACG  
AAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCC  
AGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGG  
ACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGG  
GCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCC  
AGAGAGGCCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACC  
CCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGAT  
GCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTGGTGTATGTGTGCAAGC  
CGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCCAGAGAGGTCCCCGATG  
AGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGGAGGACCTGGAGAGGAGCC  
TGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCTGCACTGCTGGGAGGGGAAG  
AGATT**TAG**ATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCA  
GGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTACATCTTCTTCCCAGTAAGTTTCC  
CCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGCTCCCCAGGCTGTTCTCCAGGC  
TTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAACTGCAGGAGCAGTTTGCCACCCCT  
GTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCGTTTGTCTACATGGCTT  
TGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTCTGATTGGTTTTGGGG  
AAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAAATGCAACAAATGAATT  
TTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGCAGATGAAATGT  
TCTGTTACACCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCCTACCTCTGT  
GCCAGGGCAGCATTTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGGAGGGGGT  
CATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCCCAAGT  
CACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCTCTC  
CACTACCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGATT  
TTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACCTAATTCTCACATCCCTCTAAAAGTAA  
ACTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAAT  
GATATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTGAAAGGTATATGACTGAGCG  
TAGCATACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGA  
AATTTGCAAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACC  
GAGCAGGGCTGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTC  
CACAAATGATGTTTTAGGTGTGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAA  
GTTTAAAGTTGCACATGATTGTATAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACAT  
AAGTTGCATTTAGAAATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAA  
AAA

**FIGURE 8**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSY PQEEATLNEMFREVEELMEDTQH  
KLRS AVEEMEAE EEA AAKASSEVNLANLPPSYHNETNTDTKVGNN TIHVHREIHKITNNQTGQM  
VFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQ RMLCTRDSECCGDQL  
CVWGHCTKMATRGSNGTICDNQRDCQ PGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLI  
TWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGS RDQDGEILLPREVPDEYEVGSFME  
EVRQELEDLERSLTEEMALGEPAAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144



**FIGURE 9**

**CGG**ACGCGTG GGGCGGACGCGTG GGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCC  
ACGGCCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCC  
AAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTCTGG  
ACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTAC  
TGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACA  
CTCCGTTACCACACTGGGTCATTGGCATTGAGGCCCTCATCCTGACCCTTGTGCAGATAGCC  
CGGGTCATCTTGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCCTGTAGCCCGCTGC  
ATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGC  
AATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTC  
ATGCTACTCATGCGAAACATTGTCAGGGTGGTCGTCCTGGACAAAGTCACAGACCTGCTGCTG  
TTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTTCTTTTTTTCTCCGGT  
CGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATC  
ATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGT  
GTGGACACGCTCTTCCTCTGCTTCCTGGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGG  
CCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAGAGGCGCCCCCGGAC  
AACAAGAAGAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGCACCCACCCCCACCGT  
CCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGTAAAAAAGGTTTTAGGC  
CAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTGAGGCGGGCGGATCACCTG  
AGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCCGTCTCTATTAAAAATACAA  
AAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTACTCGGGAGGCTGAGGCAGGAG  
AATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCACTCCAACC  
TGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAAAAGATTTTATTAAAGATATTT  
TGTTAACTC

**FIGURE 10**

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLFW  
 TLNWVLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIA  
 RVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAF  
 MLLMRNIVRVVLDKVTDLLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLP  
 MTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKNEAPPD  
 NKKRKK

**Important features:****Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310

**FIGURE 11**

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAG  
 CCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCT  
 GCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCCTGG  
 GGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCT  
 GGGTGCTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGGCTCCC  
 TGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTT  
 TCACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAGAATGGGT  
 TTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACATCCCTGACG  
 GCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCATCCTCATCC  
 AGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGCAAGGCCGAGG  
 AGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTTCTACTTGCTGT  
 CGATCGCGGCCGTGGCGCTGATGTTTCATGTACTACACTGAGCCCAGCGGCTGCCACGAGGGCA  
 AGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTCTGCCCA  
 AGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATCACCTCTACACCA  
 TGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAA  
 CCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATG  
 CCCCCAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCTCTTCATCAGTCTGCGCTCCT  
 CAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCA  
 CACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACG  
 GCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCTGGCCTCACTGCACGTCATGA  
 TGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGATGATCAGCACGTGGACCGCCG  
 TGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTCTACCTGTGGACCCTGGTAGCCC  
 CACTCCTCCTGCGCAACCGCGACTTCAGCTTGAAGGCAGCCTCACAGCCTGCCATCTGGTGCCTC  
 CTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTCCCCACACCAATCAGCC  
 AGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCCTGAGCCGGGCCTTCTAGTCGT  
 AGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCACACCCAC  
 ACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCCTGTTGCCCATACTCAGCATCTCGGATGAAA  
 GGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCCACC  
 ACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCCAGGGGACCTGCC  
 CCCTTCTGGACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCG  
 TGTAACAAAAA

**FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVES  
QLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPR  
AAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQR  
WLGKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTCVCVS  
IAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGY  
ETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRA  
FDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICASWAGLLLY  
LWTLVAPLLLRNRDFS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

**FIGURE 13**

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGT  
 GAGGTTGGAAAAAGACTCCTGTAACCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAG  
 AACGCTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCC  
 ACACAACCTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTC  
 AGGAGGACTTTCTGTTTGTGTTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATA  
 GAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTAC  
 TATTCTTCATATTTTGATATATTTCTTCTGGCAGTTTTTTCGATTTAAAGTGTTAATACTTGCA  
 TATGCTGTGTGCAGACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCC  
 TTTTACTAGCAAAAGTGATCCTTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTG  
 CCCATCATTTTCATTCATCCTTGCCCTGGATTGAGACGTGGTTCCCTGGATTTCAAAGTGTTACCT  
 CAAGAAGCAGAAGAAGAAAACAGACTCCTGATAGTTTCAGGATGCTTCAGAGAGGGCAGCACTT  
 ATACCTGGTGGTCTTTCTGATGGTCAGTTTTATTTCCCTCCTGAATCCGAAGCAGGATCTGAA  
 GAAGCTGAAGAAAAACAGGACAGTGAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTA  
 AATGTGAAAAACCCTCACAGAAAGTCATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTG  
 TCGACAGTAAAGTTGAAATGGTGACGTCCACTGCTGGCTTTATTGAACAGCTAATAAAGATTT  
 ATTTATTGTAATACCTCACAAACGTTGTACCATATCCATGCACATTTAGTTGCCTGCCTGTGG  
 CTGGTAAGGTAATGTCATGATTCATCCTCTCTTCAGTGAGACTGAGCCTGATGTGTTAACAAA  
 TAGGTGAAGAAAGTCTTGTGCTGTATTCCTAATCAAAGACTTAATATATTGAAGTAACACTT  
 TTTTAGTAAGCAAGATACCTTTTTTATTTCAATTCACAGAATGGAATTTTTTTTGTTCATGTCT  
 CAGATTTATTTTGTATTTCTTTTTTAACTCTACATTTCCCTTGTTTTTTAACTCATGCACA  
 TGTGCTCTTTGTACAGTTTTTAAAAAGTGTAATAAAATCTGACATGTCAATGTGGCTAGTTTTTA  
 TTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGACTTGCAAAAGGGGAAGAAAGG  
 AATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTTTTATCATGAAATCATGTTT  
 TTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAAATGACTTAAACC  
 ATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAAATGAACTAAATTAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDL  
LFVTLLWIIELNVNGGIENLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAI  
ALTTAVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLPPQEAEENRLLIV  
QDASERAALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

#### **N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

**FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCCGACCCGCCAGGAAAGACTGA  
 GGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCCTCCCGGGACAGAAG**ATG**TGCT  
 CCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGGGCT  
 GCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCA  
 CGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCA  
 TGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCCTGGACCTGTACAGAACC  
 AGATCGCCAGCCTGCCAGCGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGA  
 CGGCCAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCC  
 TCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCC  
 TCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCCGCTGCGCCTGCCCCGCC  
 TGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTG  
 CCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCA  
 GCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTG  
 TGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCCAGC  
 TGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCC  
 TGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCC  
 GCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGCCCCCTGGGTGCGCGAGAGCCACG  
 TCACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAAGCTGGCCGGCTGC  
 TCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACACAGCCACAGTGCCCCA  
 CCACGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGTCTTAGCTTGGCTCCTACCTGGCTTA  
 GCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGC  
 CTGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG  
 GGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCC  
 AGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGA  
 CCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAGG  
 GGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGC  
 GGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCCA  
 ACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAGGGCGAGGAGG  
 CCTGCGGGGAGGCCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCC  
 GCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCTGG  
 CTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGGACA  
 AAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCCCTTGGAGC  
 CAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGC  
 CACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGCCCTACATC**TAA**G  
 CCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTG  
 CTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGAC  
 CACAGCTGGGCCCTGTTCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGC  
 TGACGAGCCCTAACGTCCCCAGAACCAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGC  
 AACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCCCTGC  
 TGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAG  
 GGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAA  
 ACTGGAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAG  
 ATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTG  
 TAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAATAAAAGATGAAGTGTGAAA

**FIGURE 16**

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENG  
 ITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRL  
 ERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEPGIL  
 DTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRI  
 AQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRE  
 SHVTLASPEETRCHFPKPNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPT  
 WLSPTAPATEAPSPPSTAPPTVGPVPQPDQCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYC  
 ESQMGQGTRPSPTPVTPRPRLSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGP  
 DKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVT  
 QAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPAGPLELEGVKVP  
 LEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
 594-600, 640-646



**FIGURE 17**

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTC**ATG**  
 CGGGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCC  
 TCGGATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAG  
 TCAGTAAAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTCAGAA  
 GAATCTGAATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAA  
 AGTGTACAGAAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAG  
 CCAAAGAAAGTACGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGC  
 CACTTCCCTTTTCTTTTCTTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGGAAGAT  
 GGCAGACTGTGGTGTGCTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAA  
 ACTGAAGAAGAGGCTGCTAAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGA  
 ATGAAAATCCTTAATGGAAGCAATAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAA  
 AAGGCAGCAAGCATGAACCATAACCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGT  
 GATTACTTGCCACAGAATATCCAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGC  
 TCTCCCAAGGGACAGACTGCTCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGT  
 CAGGCAAAGGCTCTTGTATATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATG  
 GTTTTGGTAAGTAGACTTT**TAG**TGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTA  
 TAGCGGCCACAACTTTTTTCAGCTTTTCATGATCCAGATTTGCTTGTATTAAAGACCAAATATTCA  
 GTTGAACTTCCTTCAAATTCTTGTAAATGGATATAACACATGGAATCTACATGTAAATGAAAG  
 TTGGTGGAGTCCACAATTTTTCTTTAAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAG  
 ATCTGATAAATGGCTCTTTTTTAAATTTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTACAT  
 TAGATTATCATAATTTTAAAAATTTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATA  
 GAAAAACAACATGAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAAATTCA  
 TGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTGTTTTTTACTTTTCATGATT  
 GGCTGTCTTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTTCCAGTAGTC  
 TCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAATCATTTT  
 TTAATAAAATTATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 18**

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDS  
 EESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHGEP  
 CHFPFLLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMGEAEMMYQT  
 GMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFEKLTEE  
 GSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIHMLVLSRL

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

**FIGURE 19**

AATTCAGATTTTAAAGCCCATTCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTC  
 TTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGGAAAA**ATG**CTCTTTTGGGTGC  
 TAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAAGTAAAGATTGAAGACA  
 TCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAA  
 CTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTT  
 TAAAGGCAGAAACCTCAGAGAGACTTCGTAAGTGTGCTTCTGGATGTGACCGACCCAGAGAATG  
 TCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCA  
 ATAATGCTGGTGTTCGCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAG  
 AACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCA  
 AGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCAATCGTTGGAG  
 GGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGA  
 AAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATC  
 CAGTAAAGGTAATTGAAAAAAAGTCTAGACAACTGAAAGGCAATAAATCCTATGTGA  
 ACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAAGTCTCTTCCCTAAGA  
 CTCATTATGCCGCTGGAAAAGATGCCAAAATTTCTGGATACCTCTGTCTCACATGCCAGCAG  
 CTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAATCCCAAGGCAGT**GTAC**  
 TCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGATTTCAAGAACACATCTCCT  
 TTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGATCGTGCTTATTTGGATTGC  
 AAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTGCTCAAGTTTTCTTTGAAAAG  
 GAGGGCTGGAATGGTACATCACATAGGCAAGTCCCTGCCCTGTATTTAGGCTTTGCCTGCTTGG  
 TGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGATCTTTACCGTGGCCTGCCCA  
 TGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGTATCATCTCTTATCTAAATA  
 TTAAAGATAAGTCAACCCAAA

**FIGURE 20**

MLFWVLGLLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTE  
SGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLT  
LEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDS  
LRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKG  
NKSIVNMDLSPVVECMDHALTSLEPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELAN  
PKAV

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

**FIGURE 21**

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGG  
CGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGT  
AAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATAC  
AATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGA  
AGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTA  
CAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTT  
GCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGA  
AAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTTTCACAG  
GGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAACTGTATCAGG  
TTCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTTGAAGA  
AGATGGATCCTTAAAGGAGGTACATAAGATAAAATGAAATGTATGCTTCATTACAAGAGGAATT  
AAAGAGTATATGCAAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGT  
AAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAA  
GAACATCCAAAAAGACCCTCAGGAGAACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCC  
AAATTCTGAATTTCTTCATTTCATGTGTTATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAG  
CTGTA ACTACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAATGGTAGAACACACTGA  
CATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCATAAAGCCTTAGACTTAGA  
TGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAACGATCTAAAGCAAA  
TACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCCAGAAACAGATGAAGAAAT  
TGAAAAGATGAAGGGTTTTTGGTGAATATTCACGGTCTCCTACATTT**TGAT**CCTTTTAACCTTA  
CAAGGAGATTTTTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTT  
GAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTACCTGTTTGCAGTAATACACAGAT  
AACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCAGATGCTTTTATTTCCAAAC  
CTTTTTTTCACCTTTCACCTAAGTTGTTGAGGGGAAGGCTTACACAGACACATTCTTTAGAATT  
GGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACTTAGGGGAAGACAAGTC  
AGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATTGAGACCATGTCTA  
TTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAAGAAATTTATAT  
GAAAATTTATCTGAGTCATTAAAATTCTCCTTAAGTGATACTTTTTTAGAAGTACATTATGGC  
TAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAAATTTGCAAAACATCATCTAAAATTT  
AAAAAAAAAAAAAAAAAAAAA

**FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLEGEVKGEAKNSITDSQMDDVEVVYTIDIQK  
YIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKERRHSDQIMTFRERLLHKNLQEHFS  
NQDLVFLLLTPSIITESCSTHRLHSYLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMST  
GFSRAVQTHSSKFFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKR  
EIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNH  
HLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLLDLTQDKRSKANTGSSN  
QDKASKMSSPETDEEIEKMKGFGEYSRSPTF

**Important features:****Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

**FIGURE 23**

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCC  
 CAAGCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCCTCTGCGGTCCCCGCGGCGCCTGCCACCCTTCCCTCC  
 TTCCCCGCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTGCTGCCCCGCGAAACCCGAGGTACCAGCC  
 CGCGCCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCCTGGCCCGGCGCCTGGCACCGGGG  
 ACCGTTGCCTGACGCGAGGCCAGCTCTACTTTTCGCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACT  
 CCAACTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAGCGCCGC  
 TTCCCGTCCGGTCCCAAAGGTGGGAACGCGTCCGCCCGGCCCGCACCATGGCACGGTTCGGCTTGCCCCGCGCTT  
 CTCTGCACCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGA  
 CGTCTTTACGTGTCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATC  
 TGTCCCCAGGGTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAA  
 AGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATTCTTC  
 AAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAA  
 AATTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAA  
 ATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCCTGGTGAACCTCCAGTACCACTTTACAGAT  
 GAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCTCGCAAATTGAAGCTC  
 CAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTTCGCTCAAGGCTTAGCGGTTGCGGGAGATGTCTGAGCAAG  
 GTCTCCGTGGTAAACCCACAGCCAGTGATCCCATGCCCTGTTGAAGATGATCTACTGCTCCCACTGCCGGGGT  
 CTCGTGACTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGCTGTTTGGCCAACCAAGGGGATCTC  
 GATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGAGGGTCCTTTCAACATTGAA  
 TCGGTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGATAATAGTGTTCAGTGTCT  
 CAGAAGGTTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGTTCATCTCTGAAAGT  
 GCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACACAGCAGCTGGCACTAGTTTGGACCGA  
 CTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTCTGGTCCCTTCCGAGCAACGTTTGCAAC  
 GATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTACCTGTTT  
 GCAGTGACAGGAAATGGATTAGCCAACAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACCAGACATA  
 CTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG  
 GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCA  
 GAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCCT  
 GGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCTGGTTATGCAGAGAGAGTGGAGATTAATTCTCA  
 AACTCTGAGAAAAAGTGTTATCAAAAAGTTAAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTTGC  
 TTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTAAGAAGTGCTGACTTTGTTTTC  
 TCATTGAGTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCCAAACCATGTTAAACGTGGCT  
 AACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTTT  
 TTCTCATTTGTTTGTGGGTTTTTTTTTCCAACGTGATCTCGCCTGTTTCTTACAAGCAAACAGGGTCCCTT  
 CTTGGCACGTAACATGTACGTATTTCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATC  
 TTATTAAAAAGAAAAAGCCCAAAAAGC

**FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQG  
 STCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVK  
 TYGHLVMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEYLEC  
 VSKYTEQLKPFPGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMI  
 YCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNFNIDAMLMVAERLEGPFNIESVMDPI  
 DVKISDAIMNMQDNSVQVSQKVFQGC GPPKPLPAGRISRSESASF SARFRPHHPEERPTTAA  
 GTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKKGKSRYLFAVTGNGL  
 ANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGEGSGSGCEY  
 QQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**Important features:****Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506



**FIGURE 25**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTG  
ACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGC  
AACTTACAGCTGCACCGACAGTTGCG**ATG**AAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGC  
CACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGG  
ACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATT  
GGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCC  
CCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAA  
ACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGC  
CTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAG  
CACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACCCCTAAATCAT  
TCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTTGCTCTCTCTAGTGTCTT  
CTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAA  
GATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCATTTAACCTTAAATGCAATCAGGAAAGTA  
GCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAAAAA

amino acids 27-33, 46-52

**FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTC  
AGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCC  
TGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAGCTACTTCCCCCT  
ACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCT  
TCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCG  
GAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATC  
CCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGT  
TTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCT  
GCACTCTGGTGCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCCGGAGAGTAC  
TGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCT  
TCATGTGGCAGCAAGTTTTTCGAGCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCA  
GAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCC  
CTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCC  
CAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGC  
CTATCTATCTTCCACTGAGAGGGACCT**AG**CAGAATGAGAGAAGACATTCATGTACCACCTACT  
AGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATCCCGCCTTCGACAGTGA  
AAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCCTGTTGTATCCTCAACTG  
CAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTCCCTTTCCTTCGTTCCCAT  
GGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGTCTCTAGGAAGTGGTCACAA  
AAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCTCTCCCCACTACCACCTTCTT  
CCTGAGCTGGGGGCACCAGGAGAATCAGAGATGCTGGGGATGCCAGAGCAAGACTCAAAGAG  
GCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAAACCACG

## **FIGURE 28**

MDILVPLLQLLVLLLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIK  
GLTGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAP  
GEDMRQLADGSMDDVVCTLVLCVQSPRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAFMWQQ  
VFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPHIMGKAVKQSFSSKA  
LICSFPSLQLEQATHQPIYLPRLGT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Leucine zipper pattern.**

amino acids 10-32

#### **N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

**FIGURE 29**

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCTG  
CTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCTCT  
TCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTG  
CCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGG  
GATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGC  
CTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTT  
CATTAAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATG  
TCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 30**

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQP  
RGEGEKVG DG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

Figure 30: Amino acid sequence of the protein. The sequence is MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRGEGEKVG DG. The signal peptide is highlighted in red. The growth factor and cytokines receptors family is highlighted in blue.

**FIGURE 31**

GTTTGAATTCCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAG  
 TTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACT  
 CCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAAT**CA**  
**TG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGA  
 TGTTTACCTTCAGATTCATCACCACCCTTCTGGTTACATTTTCATTTCAATTGGTTATTTTGG  
 GATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCA  
 TAGAATTGGACACAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAG  
 GCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTG  
 AGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGT  
 GGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAA  
 CTGCAGGAGCTGCCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCCCTTTCGGGCATTC  
 GGTACATGTGGTTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCC  
 AGCAAATGACTATAGCTGGGGCAGTGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTC  
 CTGATCATCCCATCCTTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGA  
 AAGGGTCATTTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCATGTACATGCAAACG  
 CACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGATGCTGCTACTGCTGTT  
 TCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATATACTACAACCTGCTATTA  
 ATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCTTGTCCAAGAACTCAAGTC  
 ACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTAGGAAAGGTGTTAGTGGTGT  
 GTTTCATGTTTTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCCAGGTGTGGGCAG  
 TCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGCCCATAGTTTTTTTATCTGTGTTTG  
 AAATGTGCTGGATGCACTTTTCCTGTGTTTTGCTGTTGATCTGGAAACAAATGATGGATCGT  
 CAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTAAAAAGGAGCAACAAATTAA  
 ACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGAGGGGAACAGAACTCCAGG  
 CCATTGTGAGAT**TAG**ATACCCATTTAGGTATCTGTACCTGGAAAACATTTCTTCTAAGAGCCA  
 TTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTTTTTAAAGACCTAA  
 TAAACCCTATTCTTCCTCAAAA

**FIGURE 32**

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYYDYTNDLS  
IELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPL  
WTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILAC  
QQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQN  
ALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSS  
HFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFSLVF  
ETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQ  
AIVR

**Important features:****Signal peptide:**

amino acids 1-20

**Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

**N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

**N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348



**FIGURE 33**

[illegible]

**FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCP  
 AGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSL  
 PRWRESFIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPPIPGTTAQPVTLMQLLA  
 VTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQRQDP  
 SGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQL  
 LADVAQALDIGPAGPLMGVVQYGDNPATHTNLKTHTNRDLKTAIEKITQRGGLSNVGRAISF  
 VTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVV  
 EPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVVKRVCDTDLACSKTCLNSADIGFVIDGSS  
 SVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLFEFGFDKYSSKPDILNAIKRVGY  
 WSGGTSTGAAINFALQFLFKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAW  
 AAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

**Important features:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
 431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

**FIGURE 35**

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAA  
 GAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTT  
 TAATTAAGCATGGAATACAGAAAACAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATTCCA  
 CAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCAC  
 GTGGTGCTCTCCGACTACTCACCCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTGAGCTG  
 CTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCCCTCAAA  
 TGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCTTCCCCAC  
 TACAATGTGATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTTACAGACAA  
 GACTTTCAC TTCACACTTCGAGAGCATTCAAACCTGCTCTCATCAAAATCCATTTCTGGTCATT  
 CTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGT TACTTGGGGTGAA  
 AAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAG  
 GAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGA  
 CAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCAT TATGGCATT CAGGTGGGTA  
 ACTGAGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTTTCATCAATACT  
 GGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTTTTCACAGGTTATCCT  
 CTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTTCTTACCAGGAGTAT  
 CCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGT TATATAATGTCCAGAGATTTGGTG  
 CCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTTGAAGATGTTTATGTCGGG  
 ATCTGTTTGAATTTATTAAAAGTGAACATTCATATTCCAGAAGACACAAATCTTTTCTTTCTA  
 TATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCC  
 AAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACTTCAC  
 ATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTG  
 TGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACTGAACTGAACTCATGAAAAACCCA  
 GACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGGCCCTTCAAAGATGATATGTGG  
 AGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGGACCAACAATTTG  
 GACATGTCA T TCTGTAGACTAGAATTTCTTAAAAGGGTGTTACTGAGTTATAAGCTCACTAGG  
 CTGTAAAAACAAAACAATGTAGAGTTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTTGT  
 GTATATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAAACTTCTTCA  
 CTGAAGTTATACTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTT  
 GCAGTATTTACAGTTATTATTATTTAAAAT TACTTCAACTTTGTGTTTTTAAATGTTTTGAC  
 GATTTCAATACAAGATAAAAAGGATAGTGAATCATTCTTTACATGCAACATTTTCCAGTTAC  
 TTAAGTATGATCAGTTTATTATTGATACATCACTCCATTAATGTAAAGTCATAGGTCATTATTGC  
 ATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGTAATATAGAGAAGAATTAAAG  
 CAAGAAAATCTGAAAA

**FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDF  
HFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEEKED  
KMLALSLEDEHLLYGDIIRQDFLDTYNNLTCLKTMAFRWVTEFCPNAKYVMKTDVDFINTGN  
LVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYCSGLGYIMSRDLVPR  
IYEMMGHVKPIKFEDVYVGICLNLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKE  
IITFWQVMLRNTTCHY

**Important features:****Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277

**FIGURE 37**

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCT  
TCTCATCTCGTCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAATATCATGTG  
TCGGGAGTGCTGTGAATATGATCAGATTGAGTGCCTCTGCCCCGAAAGAGGGAAGTCGTGGGTTATACCATCCC  
TTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAAGTCAA  
GAGCTGCCGAAATGGCTCATGGGGGGGTACCTTGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCG  
AGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGGA  
AAGCTATCCCCATAAATGCTCACTGTGAATGGACCATTATGCTAAACCTGGGTTTGTATCCAATAAGATTTGT  
CATGTTGAGTCTGGAGTTTGAATACATGTGCCAGTATGACTATGTTGAGGTTCTGTATGGAGACAACCGCGATGG  
CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCACGTCCT  
CTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTTCATGCCATTTATGAGGAGATCACAGCATGCTCCTCATC  
CCCTTGTTTCCATGACGGCACGTGCGTCCTTGACAAGGCTGGATCTTACAAGTGTGCCTGCTTGGCAGGCTATAC  
TGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCTGGGGGGCCAGTCAATGGGTACCAGAA  
AATAACAGGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTGGCACCGTGGTGTCTTTCTTTTGTAACAA  
CTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGGAAACAGCCCATCTG  
CATAAAAGCCTGCCGAGAACCATAAGATTTTCAACCTGGTGAGAAGGAGAGTTCTTCCGATGCAGGTTCACTCAAG  
GGAGACACCATTACACCAGCTATACTCAGCGGCCCTTCAAGCAGAACTGCAGAGTGGCCCTACCAAGAAGCC  
AGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACC  
CTTCTACCGCCGCCCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCCTG  
CATCCCTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGACCCAAGGGTTGCGCTGGCCGTGGCAGGCAGC  
CATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGGTTCCTAGTCTGCAGCGGTGC  
CCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAGGTCAACATGATCAAGAC  
AGCAGACCTGAAAGTTGTTTTGGGGAAATTTCTACCGGGATGATGACCGGGATGAGAAGACCATCCAGAGCCTACA  
GATTTCTGCTATCATCTGCATCCCACTATGACCCCATCCTGCTTGATGCTGACATCGCCATCCTGAAGCTCCT  
AGACAAGGCCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAGTCGGGATCTCAGCACTTCCTTCCA  
GGAGTCCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACT  
GCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAG  
TGTCAGTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGG  
CATCGCGGCTGTGTCTTCCCGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAG  
CTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCTTACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAAG  
AAATATGAAATGAACCATGCTCATGCACCTCCTTGAGAAGTGTTTCTGTATATCCGTCTGTACGTGTGTATTGCG  
TGAAGCAGTGTGGGCCTGAAGTGTGATTTGGCCTGTGAACCTGGCTGTGCCAGGGCTTCTGACTTCAGGGACAAA  
ACTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCGTCCACTACTAGGACAGCCAATTGGAA  
GATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAAGAAGACCATATACAAAACCTCTCCACTCCACTGACCTGGT  
GGTCTTCCCCAACTTTTCAATTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAGGCCCTTT  
TGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTTT  
GTGTACATGGCCACAGTACAGTCTGGTCCTTTTCTTCCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTG  
GCTTCTGAACCTACAA  
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## **FIGURE 38**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVG  
 YTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCM  
 RCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDN  
 RDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFAIYEEITACSSSPCFHDGTCVL  
 DKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVVSFFC  
 NNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAA  
 FSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS  
 CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAH  
 CVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLL  
 DKARISTRVQPICLAASRDLSTS FQESHITVAGWNVLADVRSPGFKNDTLRSGVVSVDLLC  
 EEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLGLVSWSY  
 DKTCSHRLSTAFTKVLPPFKDWIERNMK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **EGF-like domain cysteine pattern signature.**

amino acids 260-272

#### **N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

#### **N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
 474-480, 491-497, 638-644, 666-672

#### **Amidation site.**

amino acids 56-60

#### **Serine proteases, trypsin family.**

amino acids 489-506

#### **CUB domain proteins profile.**

amino acids 150-167

**FIGURE 39**

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTA  
ATCTGAAGGTTCTCAGTCAAATTCCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTT  
GGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGC  
TTCTGTTGCTGGTCTTGCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATT  
CAGAACTCTGTAAAGGTGCCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAG  
ACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAG  
ACGAGCCTGGCCTAGACAACCCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACT  
CTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA  
ATCGAGCTTTGAGTGTTCTTCGAAGGACAAAGAGCGGGAGTGCAAGTTGCCAACCATGCCGACCAGGGCAGGGAAA  
ATTCTGAAAACACCACTGCCCTGAAGTCTTTCGAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCA  
TCAAGATCAATCGAGTAGATCCCACTGAAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCC  
ATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTC  
TAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGG  
TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCAGCAGGAACAATGGACAGGCCCCGGATGCCTACAGAC  
CCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAATAAACTGGTGCGCA  
AGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG  
AGAATGACCGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAGAAAGTGCGGCTCATCTGATTTC  
AGGCCAGTGAAAGACGTGTTACCTCGTCGTGTCGCCAGGTTCCGCAGCGGAGCCCTGACATCTTTCAGGAAG  
CCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACTCCCAAGCCCCCTCCATCCTA  
CAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCGGCATGACCGTCGACGGGG  
GAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTTGAGCCCGGAGGAGTCATAAGCAGAGATG  
GAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTGAAGTACAGAGGTGAGCCGGAGTGAGGCAG  
TGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGCCCCAGGAAG  
ACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCTGGGTCA  
TGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG  
GCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTTTTTTCATCAAATCCATTGTTGAAGGAA  
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAA  
TGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTG  
GCACTTTTTTTATAGAATCAATGATGGGTGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACT  
ATATTTATCTTGTGATTTTTTATATTTAAAGAAAGAATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAA  
TGAAAGCCAGTTACACCTCAGAAAATATGATTCAAAAAAATTAATACTACTAGTTTTTTTTTCAGTGTTGGAGGAT  
TTCTCATTACTCTACAACATTGTTTATATTTTTTCTATTCAATAAAAAGCCCTAAAACAATAAATGATTGATT  
TGTATACCCCACTGAATTCAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTAT  
GGCCATTTTTTAATTTACAGCTAAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAAT  
AAATATTTTTTCAGAAGTTAAA

**FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATA  
 PSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSEFK  
 KINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSES  
 LSIRLVGGSETPLVHIIIIQHIIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPC  
 QVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFIENV  
 LDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQSPDIFQE  
 AGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPPIYV  
 ISVEPPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQED  
 CSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGN  
 KPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
 467-473, 603-609



**FIGURE 41**

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAA  
 GCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACCATGGGCTT  
 CAACCTGACTTTCCACCTTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCTGAC  
 AGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTTAAAGCAAA  
 GGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGA  
 AGCATCCACGAAGAAGGTAGAACTTGACAACTGTCCTTCTGTGTCTCCTTACCTCAGAGGCCA  
 GAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATCCCAAAGT  
 GTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATCCTCGTTCC  
 CCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTTCTGCAGAG  
 GCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGTTTAAATCGAGC  
 CAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGACTGCTTTATATT  
 CCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAGCATCCCAA  
 GCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGGGGG  
 TGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACTACTGGGG  
 ATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCG  
 GCCCCTGCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGT  
 GAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAG  
 TAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGA  
 TTTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGGAGAAGTGAATCTTTGTTT  
 GCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTAAGAACCTGTTACAGCTCAT  
 GTTGAGCTGAATTTTTCCTTTTGTATTTTCTTAGCAGAGCTCCTGGTGATGTAGAGTATAAA  
 ACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATGAGGGTTAAATATTGTAATATGG  
 ATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAAAATGAACGCTATTTGAGGACT  
 CTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGATAAAAGGCCACAGGAAA  
 TAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAAAGGTACGAAGA  
 TACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGTGAGAAG  
 GCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTTGGGAATGAAGAG  
 GTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGA  
 TAGCCTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTC  
 TCTATTAGTTTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGT  
 TTACAAGTTTACATATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAATGTG  
 AAAAAGCAAAA

**FIGURE 42**

MGFNLT FHLSYKFRL LLLLL TLCLTVVGWATS NYFVGAIQEIPKAKEFMANFHKT LILGKGKTL  
TNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAI  
LVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDC  
FIFHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNN  
YWGWWGEGDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTD  
GLSSCSYKLVSVEHNPLYINITVDFWFGA

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

[illegible][illegible]

## **FIGURE 44**

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMMPMFQRRRRRDTHF  
PICIFCCGCCHRSKCGMCCKT

### **Important features:**

#### **Signal peptide:**

amino acids 1-24

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

#### **N-myristoylation site.**

amino acids 44-50

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

44/168

**FIGURE 45**

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAAT**ATG**GCTGGTTCCCCAACATGCCTCAC  
CCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGT  
CGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTAT  
TGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAACAGCCAGAAGGGGGCACTATCATAGT  
GACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAG  
CAAACGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCA  
GCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCAT  
GGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGG  
GGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGG  
GTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAG  
GAACCCTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGC  
TGATGACCCAGATTCCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCT  
CTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGA  
GAAGAAGAGAGTGGACATTTGTCTGGGAACTCCTAACATATGCCCCATTCTGGAGAGAACAC  
AGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGATCCAGCAAATACGGT  
TTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCACTGCTCACGATGCCAGA  
CACACCAAGGCTATTTGCCTATGAGAATGTTATC**TAG**ACAGCAGTGCCTCCCCTAAGTCTCT  
GCTCA

**FIGURE 46**

MAGSPTCLTLIYILWQLTGSAAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTI  
QPEGGTIIIVTQNRNRERVDVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYE  
HLSKPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGES  
DMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKR  
ERQEEYIEKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIPKKMEN  
PHSLLTMPDTPRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

**FIGURE 47**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCA**ATG**ACCTGCTGCGAAGGATGGACATCCTGCAAT  
GGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTC  
AGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCA  
GGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAA  
AGAGCGTGCTGCAACAACAGAAGTGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTC  
ATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGT  
AATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCAT  
CCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAAT  
AAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCT  
GAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCTTGTTGGAATT  
CTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTC  
TCTAAGCGAAGAAGTCAAATTGTG**TAG**TTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGA  
AAAAAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAI  
 PATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNANC  
 EFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHF  
 SVFLGLLL VGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

### **Important features:**

#### **Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

#### **N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

#### **N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

#### **TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12



**FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGT  
GAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGA  
GCAGATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCTCGAA  
CTGTGAC**ATG**GAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGC  
CAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAG  
CGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATG  
CAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACATCATCAC  
TCCAGGCTCTGCCACTACTTGCT**TGA**GCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAAC  
ACTGGCCCCCAGCACCTCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGG  
GCAGGCTGTTAGGCCCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACC  
CCCTCA

**FIGURE 50**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKY  
KSSQKQHSPVPEKAIPLITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

**FIGURE 51**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAG  
 GGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGC  
 AAGGAGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAAG  
 TTCCAGGGGGCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCC  
 CTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGA  
 GACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCT  
 AAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTT  
 CCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGA  
 AACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTCGACACGGAGCAGATGCTGTC  
 CGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGGAGGCCATGGC  
 ATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACT  
 CCGTGGGTCCACGGATAACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCT  
 CCCTGGGGTCAAGGAGGCAATGGAGGGGCCACCAAACCTTGGGACCAACACTCAGGGAGCTGTG  
 GCCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCCA  
 CCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGC  
 AGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGC  
 AGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTGGTGGCAGCAGTGGCAAC  
 AGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCCTGGGGATCCAGCACCGGCTCCTCC  
 TCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACCCGGGTGTGAAAAGCCAGGG  
 AATGAAGCCCGCGGGAGCGGGGAATCTGGGATTCAGGGCTTCAGAGGACAGGGAGTTTCCAGC  
 AACATGAGGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGGAGGCTCTGGAGACAATTATCGG  
 GGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTTGGTGGAGTCAATACTGTGAAC  
 TCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAAGAATTTTAAATCCAAGCTG  
 GGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTCGCATCCCGTGAACCTCCA  
 GACAAGGAGCCACCAGATTGGATGGGAGCCCCCACACTCCCTCCTTAAAACACCACCCTCTCA  
 TCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAAAAAAAAAAAAAAAAA  
 AA  
 AA

**FIGURE 52**

MKFQGPLACL LLLALCLGSGEAGPLQSGEESTGTNIG EALGHGLGDALSEGVGKAIGKEAGGAA  
 GSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGAD  
 AVRGSWQGVPGHSGAWETSGGHGIFGSQGG LGGQGQGNPGGLGTPWVHGYPGNSAGSFGMNPQ  
 GAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQS  
 GSSGSGSNGDNNNGSSSGGSSSGSSSGSSSGGSSGGSSGGSSGNSGSGSRGDSGSESSWGSSTG  
 SSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLLGSGDN  
 YRGQGSSWGSGGGDVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

**FIGURE 53**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCT  
GGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCT  
GGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTGGCGCCGGCTCCAGT  
GTTTCCCACAGCCCCCAAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAG  
AGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGTATGGC  
TGGGTCCCATCATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATG  
CCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAG  
AAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCCGCT  
TCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTG  
ACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCC  
TCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTGTCAGGAGAGGC  
CCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATA  
TCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCT  
GCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCGCACCCTCCCCACTC  
AGGGTATTGATGATTTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGGATTTTCATTGATGTGC  
TTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGATATAAGAGCAGAGGCTG  
ACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTCCTGGGTCTGTACAACC  
TTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGCAAGAGCTTCTGAAGGACC  
GCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCCTTCCTGACCATGTGCGTGA  
AGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCGATGCTGCACCCAGGACATTG  
TTCTCCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCCTCATCGATATTATAGGGGTCC  
ATCACAACCCAACTGTGTGGCCGATCCTGAGGTCTACGACCCCTTCCGCTTTGACCCAGAGA  
ACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTCCGCAGGGCCCAGGAAGTGCATCG  
GGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGATGCTGCTGCACTTCCGGT  
TCCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGCGCGCCGAGGGCGGGC  
TTTGGCTGCGGGTGGAGCCCCCTGAATGTAGGCTTGCAAGTGAATTTCTGACCCATCCACCTGTT  
TTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

**FIGURE 54**

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFQPPKRNWFWGH  
 LGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIR  
 FLKPWLGEKILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRL  
 DMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHD  
 GRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDLFDVLLLSKDEDEGKALS  
 EDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEWDDLAQL  
 PFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYD  
 PFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLEL  
 IMRAEGGLWLRVEPLNVGLQ

**Important features:****Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

**FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTC**ATG**GGACCAGTGAAACAGCTGAAGCGAATGTTT  
GAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCT  
GCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTG  
ACGTGGTACAGCCTTTCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTTTTGCCGTG  
TGTCTTGCA**TAA**TTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGT  
GGACAGTTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGC  
AATGTGTTGCTTGTGATTTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAA  
CCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAATCTTCCTC  
ATGTACCTGTTTTCTCTCTGGATGTTGTCCCCTGAATTCCCATGAATACAAACCTATTTCAGC  
AACAGCAA  
AAAAAAAAAAAAAAAA

Figure 55: DNA sequence alignment showing a mutation (ATG) and a stop codon (TAA) in the context of a gene. The sequence is aligned with a reference sequence, and the mutation is highlighted in bold. The stop codon is also highlighted in bold. The sequence is shown in a standard font, and the mutation is shown in a bold font. The stop codon is shown in a bold font. The sequence is shown in a standard font, and the mutation is shown in a bold font. The stop codon is shown in a bold font.

**FIGURE 56**

MGPKVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGALIFCIIQLSLALTWYSLSFIFP  
ARDAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72



**FIGURE 57**

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCCGCCAAC**ATG**CTCTGTCTGTGC  
CTGTACGTGCCGGTTCATCGGGGAAGCCAGACCCGAGTTCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTG  
AAGTCCATTTTCAAGCTCAGTGTCTTCATCCCCCTCCAGGAATTCTCCACCTACCGCCAGTGGGAAGCAGAAAATT  
GTACAAGCTGGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAG  
AAGAAGCTGAGGCTGGTGTTTAAGATTTTGGACAAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATGCAG  
TCCCTGCGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTCTCAAGAGCATGGATAAAAAACGGC  
ACGATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCTCCACCCCGTGGAAAACATCCCCGAGATCATC  
CTCTACTGGAAGCATTCCACGATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAG  
AGGCAGACGGGGATGTGGTGGAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCC  
CCCCGGACAGGCTCAAGGTGCTCATGCAGGTCCATGCCCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTC  
ACTCAGATGATTTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGCAATGGCATCAACGTCTCAAAATTGCCCCC  
GAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCCTTGTTGGTAGTGACCAGGAGACTCTGAGGATT  
CACGAGAGGCTTGTGGCAGGGTCTTGGCAGGGGCCATCGCCCAGAGCAGCATCTACCCAATGGAGGTCTGAAG  
ACCCGGATGGCGCTGCGGAAGACAGGGCCAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCCTGCCAGAGAG  
GGGGTGGCCGCTTCTACAAAGGCTATGTCCCAACATGTGCAGTGAACAGCGCGGACCCCGGCGTGTGTGTCTC  
GTCTACGAGACGCTCAAGAATGCCTGGCTGCAGCACTATGCAGTGAACAGCGCGGACCCCGGCGTGTGTGTCTC  
CTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGGCCAGCTACCCCTGGCCCTAGTCAGGACCCGGATG  
CAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTCTTCAAACATATCCTGCGGACCGAG  
GGGGCCTTCGGGCTGTACAGGGGGCTGGCCCCCACTTCATGAAGGTTCATCCAGCTGTGAGCATCAGCTACGTG  
GTCTACGAGAACCTGAAGATCACCCCTGGGCGTGCAGTTCGGG**TGA**CGGGGGGAGGGGCCCGCCGCGCATCG  
CTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTTCTGTGAATGTGCCAACACTAAGCTGTCTCGAGCC  
AAGCTGTGAAAACCTTAGACGCACCCGACGGGAGGGTGGGGAGAGCTGGCAGGCCCCAGGGCTTGTCTGTGACC  
CCAGCAGACCTCCTGTTGGTTCCAGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTCAAGGGCTCCGGGCT  
CACATGTGTAAGGACAGGACATTTTCTGCAGTGCCTGCCAATAGTGAGCTTGAGCCTGGAGGCGGCTTAGTTT  
TTCCATTTTACCCTTGCAGCCAGCTGTGGCCACGGCCCCCTGCCCTCTGGTCTGCCGTGCATCTCCCTGTGCCCT  
CTTGCTGCCCTGCTGTGCTGAGGTAAGGTGGGAGGAGGGCTACAGCCACATCCCACCCCTCGTCCCAATCCC  
ATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCCTGACTTCCCAACCTACAGCATTGACGCCAACTT  
GGCTGTGAAGGAAGAGGAAAGGATCTGGCCTGTGGTCACTGGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCG  
GGCATGCTTGGGAGTGCAGGGGGCTCGGGCTGCCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTG  
CTCTGAGCTGGCCTGGACCCTGTGAGGATGGGCCCCACCTCAGAACCAACTCACTGTCCCCACTGTGGCATGAG  
GGCAGTGGAGCACCATGTTTGAGGGCGAAGGGCAGAGCGTTTGTGTGTTCTGGGGAGGGAAGGAAAAGGTGTTGG  
AGGCCTTAATTATGGACTGTTGGGAAAAGGGTTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGC  
TTCCAGAGGAAGACGAGGGAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTTCTGT  
CAACCCAGCAGGGGCGCAGCGGGACCGCCACATTTCCACTTGTGTCACTGCTTGAACCTATTTATTTTGT  
TTTATTTGAACAGAGTTATGTCTTAACATTTTTTATAGATTTGTTTAATTAATAGCTTGTCAATTTTCAAGTTCAT  
TTTTTATTCATATTTATGTTTCATGGTTGATTGTACCTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAA  
GGGGGGCCTTGGGCCGCTGCAGTCACATCTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAG  
AAGGCAGCAGCCCTGGCTCCTTTTCTTTGGCAGGTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTTTCAAGGTTT  
GACTGGGGGCGTGGAGAGAGAGGGAGGAACCTCAATAACCTTGAAGGTGGAATCCAGTTATTTTCTGCGCTGCGA  
GGTTTTCTTTATTTTCACTCTTTTCTGAATGTCAAGGCAGTGAAGTGCCTCTCACTGTGAATTTGTGGTGGGCGGG  
GGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGTCCCTCCAGCCTTCTGCTGCCCTTGCTTAACAATGCCGGCCAA  
CTGGCGACCTCACGGTTGCACTTCCATTCCACCAGAATGACCTGATGAGGAAATCTTCAATAGGATGCAAAGATC  
AATGCAAAATTGTTATATATGAACATATAACTGGAGTCGTCAAAAAGCAAATTAAGAAAGAATTGGACGTTAGA  
AGTTGTCATTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 58**

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDL  
DGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILKSM  
DKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMWWRH  
LVAGGGAGAVSRTCTAPLDRKVLMMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLK  
IAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMALRKTGQ  
YSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVF  
VLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFLYRGLAP  
NFMKVIPAUSISYVVYENLKITLGVQSR

**Important features:****Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140



**FIGURE 60**

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIK  
LSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAG  
TYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGA  
NFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTSEIKRRSHLQ  
LLNSKASLCVSSFFAISWALLPLSPYMLK

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

**FIGURE 61**

TGACGTCAGAATCACC**ATG**GCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACA  
 AGCACCAGGAGCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGG  
 TAGTGGGCTACCCCCTGGTGGTGGTTATGGGGGTCCTGCCCCTGGAGGGCCTTATGGACCACC  
 AGCTGGTGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCCTCTGGAACCTCCAGGAGG  
 ACCATATGGCGGTGCAGCTCCCGGGGGCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGC  
 CCAGCAGCCTGGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTACTC  
 CTGGTTCCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGC  
 CCTGGTCAACTGCAATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTT  
 TGACAAGACCAAGTCAGGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCA  
 GCAGTGAAGAACCTCTTCCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGA  
 GCTGCAGCAAGCTCTGTCCCAAATGGGCTACAACCTGAGCCCCCAGTTCACCCAGCTTCTGGT  
 CTCCCGCTACTGCCCCAGCTCTGCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTG  
 CACCCAGCTGCAGGTGCTGACAGAGGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACAT  
 CCGGCTCAGCTTCGAGGACTTCGTACCATGACAGCTTCTCGGATGCTAT**TGA**CCCAACCATCT  
 GTGGAGAGTGGAGTGCACCAGGGACCTTTCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACA  
 TCTCTTCTTTTCTGTCCCTCTAGAAGAACATTCTCCCTTGCTTGATGCAACACTGTTCCAAA  
 AGAGGGTGGAGAGTCCTGCATCATAGCCACCAAATAGTGAGGACCGGGGCTGAGGCCACACAG  
 ATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGAATGTCCTGATGGCCATGAGCAGTTGAGTG  
 GCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCA  
 CCCTGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACCGTTAGTACCTGTGTTCCCTCACCAG  
 GCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGGAATCTGACCAAGCATGAGAGAGATCT  
 GTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAATCCTTGTGTGTTAACTTCTAGC  
 TGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCATCTTTGGCCAGGCTTCTGCC  
 CCCTGCAGCTGGGACCCCTCACTTGCCCTGCCATGCTCTGCTCGGCTTCAGTCTCCAGGAGACA  
 GTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTTTCATTTGGGGCCAAAAG  
 TCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

**FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGP  
YGHPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSV  
DSDHSGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNL  
FQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQV  
LTEAFREKDTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-  
66, 70-75, 78-83, 83-88, 87-92, 110-115

**FIGURE 63**

CAGG**ATG**CAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCA  
TCTCCCAGGCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGG  
GACCAACTTGCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCA  
GCCCCGCTCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCCTCTGAAGCTCAGCGTGCCTCC  
ATCAGATGGCTTCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCT  
GCCTGCCATGGATTCTTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGA  
CCGCTGGGGGAAGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGCTGCGGGCCCTCGCTCC  
GGGCAGTGGCCCTTTGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTC  
ACTCTCCACCAGGACTCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGG  
AAAAATCCTTTCCCAACGCCCTCCCTGGTCTCTCATCCACAGGGTTCTGCCTGATCACCCCTG  
GGGTACCCTGAATCCCAGTGTGTCTTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAG  
GCCCCATGCCACACCCTGAGGGAATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGG  
AAATATTAATCGGTATCCAGGAGGCAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTG  
GGGGAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTCATCTATACCCAGGTATCAA  
TAACCCATTTCTCCTGGAGTTCTCCGCCCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTT  
CCCTAATCCTCCAAGCCCTAGGTTGCAGTGGGGC**TAG**AGCACGATAGAGGGAAACCCAACATT  
GGGAGTTAGAGTCTTGCTCCCGCCCCCTTGCTGTGTGGGCTCAATCCAGGCCCTGTAAACATGT  
TTCCAGCACTATCCCCACTTTTCAGTGCCTCCCCCTGCTCATCTCCAATAAAATAAAAGCACTT  
ATGAAA  
AAA

**FIGURE 64**

MQGRVAGSCAPLGLLLVLCLHLPGLFARSIGVVEEKVSNFGTNLPQLGQPSSTGPSNSEHPQP  
ALDPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAAEDR  
LGEALPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGK  
ILSQRPPWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTSWG  
INRYPGGSWGNIINRYPGGSWGNIINRYPGGSWGNIHLYPGINNPFPFPGVLRPPGSSWNIPAGFP  
NPPSPRLQWG

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310



**FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GGG  
TCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGT  
ATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTC  
CTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTC  
CACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTGTGTCC  
TTCTTGGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAG  
GCCCCACCCCTCCTGAGTGGCAATAAATAAAATTTCGGTATGCTG

**FIGURE 66**

MGSGLPVLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTSV  
TLHHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

**FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGG  
GCCAGGTGCCCCGTGCGAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAG  
CCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTT  
CTGGCGCTGGGCCTGCCGTTCTTGCTGGCCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACC  
ACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAAC  
CTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTG  
GCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGGCACCTAC  
CGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCTCAGGACTCCAAG  
GAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCTCTCCTGCATCTGTCTCCCTTCATTGC  
TGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAG  
CAGGGAAGAAGGTACTTCAAAGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTT  
TTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIVV  
FSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32

### FIGURE 69

[illegible]

**FIGURE 70**

MGLFRGFVFLLVLCLLHQSNSTFIKLNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTASTYL  
FEATEKRFFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGE  
KGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCSA  
GISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVEFCNE  
KTHNQEAPSLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPPVFSLLKISQRIVCLVLDKSG  
SMGGKDRLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTY  
PLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDEDNTASSCIDEVKQSGAIVHFIALGRA  
ADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMN  
DTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGTWAY  
NLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQGYVPVLGANVT  
AFIESQNGHTEVLELLDNGAGADSFKNDBGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRP  
PLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLEDFSRASGGAFVVSQVPSLPLPDQYPPS  
QITDLDATVHEDKIIILTWTAPGDNFVDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKE  
ANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPT  
PTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

**FIGURE 71**

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGGCAGGGG  
 TGACAACAGGTGTCATCTTTTTGATCTCGTGTGTGGCTGCCTTCCTATTTCAGGAAAGACGCCAAGGTAATTTT  
 GACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCAGTTATGCCAGGATTTACTAG  
 AGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTTGGTGGAGGAGAGAACCTTTGTGGGGCTGC  
 GTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAGAAAGGAAAGGTCCCCTCTTGCTGTTG  
 GCTGCACATCAGGAAGGCTGTGATGGGAATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCT  
 GCAAGATCATCTTTAAAAGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAA  
 GGAAATGGATGCAAGCAGCTCCGGGGGCCCCAAACGCATGCTTCCTGTGGTCTAGCCAGGGAAGCCCTTCCGTG  
 GGGGCCCGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGGTTCGCCGGGGG  
 CTGCTTGGCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGCTCCTCTGCTGTGCTATCTCTGTCTGTACATGTTG  
 GCCTGCACCCCAAAAGGTGACGAGGAGCAGTGCCACTGCCAGGGCCAACAGCCCCACGGGGAAGGAGGGGTAC  
 CAGGCCGTCTTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTC  
 AAGGAGGAGCTGCAGGAGAGGAGTGAAGCAGCTCAGGAATGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGT  
 CTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTCCTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAG  
 GTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTGCCCTTCGATAGCTTTACTCTACAGAAGGTGTAC  
 CAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGATGAGTTGGTGGAA  
 GCCATTGAATCAGCCTTGGAGACCCTGAACAATCCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCTCT  
 GATTTCATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAAAGGGGACCAC  
 AAACACGAATTCAAACGGCTCATCTTATTTTCGACCATTTCAGCCCCATCATGAAAGTGAAAAATGAAAAGCTCAAC  
 ATGGCCAAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAAGTTCCGGCAGTTTCATGCAGAAT  
 TTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGGAAAGAAGAAATAAAT  
 GAAGTCAAAGGAATACTTGAAGAACCTTCAAAGCTGCCAAGCTTCAGGAACCTTACCTTCATCCAGCTGAATGGA  
 GAATTTTCTCGGGGAAAGGACTTGATGTTGGAGCCGCTTCTGGAAGGGAAGCAACGTCCTTCTCTTTTTCTGT  
 GATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAGGTATTT  
 TATCCAGTTCTTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAG  
 CAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTCACTATCGGTGAGAC  
 TTCAATCAATAGGTGGGTTTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTATCGCAAGTAT  
 CTCCACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTCCACCTCTGGCATGAGAAGCGCTGCATG  
 GACGAGCTGACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTG  
 GGATGCTGGTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAAAACAGAAACAGAAAGACAAGTAGCAAAAAACA  
**TGA**ACTCCAGAGAAGGATTGTGGGAGACACTTTTTCTTTCCTTTTGCAATTACTGAAAGTGGCTGCAACAGAGA  
 AAAGACTTCCATAAAGGACGACAAAAGAATTGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGT  
 TGGGCTTTTACAAACAGAAATCAAAATCTCGCTTGCCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGCT  
 GACAAAGGCAGAATGCTTGTGAGATTATAAGCCTAATGGTGTGGAGGTTTTGATGGTGTTTACAATACACTGAGA  
 CCTGTTGTTTTGTGTGCTCATTGAAATATTATGATTTAAGAGCAGTTTTGTAAAAAATTCATTAGCATGAAAGG  
 CAAGCATATTTCTCCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTCTAGGAATGCTAAAATATCAGAAGG  
 CAGGAGAGGAGATAGGCTTATTATGATACTAGTGAGTACATTAAGTAAAAATAAAATGGACCAGAAAAGAAAAGAA  
 ACCATAAATATCGTGTGCATATTTTCCCCAAGATTAACCAAAAATAATCTGCTTATCTTTTGGTTGTCCTTTTAA  
 CTGTCTCCGTTTTTTTTTATTTAAAAATGCACTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTAC  
 CACTTTGCAAGCCTTACAAGAGAGCACAAAGTTGGCCTACATTTTTTATATTTTTTAAGAAGATACTTTGAGATGCA  
 TTATGAGAACTTTTCAGTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAATGCTGATTCTGTGAGGC  
 ACTGAATGTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGACGTACAGATACTTTCTCTGAAG  
 AGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAAAAGGAACT  
 CATTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACATTTCTCCTCAGAAGTAGGGACCGCTTT  
 CTACCTGTTTAAATAAACCAGATATACCGTGTGAACCAACAATCTCTTTTCAAAACAGGGTGCTCCTCCTGG  
 CTTCTGGCTTCCATAAGAAGAAATGGAGAAAAATATATATATATATATATATATTGTGAAAGATCAATCCATCTG  
 CCAGAATCTAGTGGGATGGAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAGTAACTGAATTATTTT  
 TTAATTAAGCAGTTCTACTCAATCACCAAGATGCTTCTGAAAATTGCATTTTATTACCATTTCAAATATTTTT  
 TAAAAATAAATACAGTTAACATAGAGTGGTTTTCTTATTGATGTGAAAATTATTAGCCAGCACCAGATGCATGAG  
 CTAATTATCTCTTTGAGTCTTGTCTTGTGTTGCTCACAGTAACTCATTTGTTTAAAGCTTCAAGAACATTCAA  
 GCTGTTGGTGTGTTAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTTAATTAACACAGGCCA  
 TGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

**FIGURE 72**

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQE  
WEEQHRNYVSSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHS  
QVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALE  
TLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVK  
NEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILEN  
TSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPG  
KKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDL  
DIKGWGGEDVHLYRKYLHSNLIVVRTPVRLFLHLWHEKRCMDELTPEQYKMCMQSKAMNEASH  
GQLGMLVFRHEIEAHLRKQKQKTSKKT

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381



**FIGURE 73**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGATC  
CAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGC  
AAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCA  
CTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCCTCTAGTCCTCAAATCCCAGTCCCCTGC  
ACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCCTGGCT  
GCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCAGCCTCT  
TACCCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTT  
GACCCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTTGGAC  
CTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTT  
CCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCACTGGGGTCAGAAAGGATCCCCAGGGGGG  
TCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTACATTATGACTCT  
GATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGGCATC  
CTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAA  
GTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAA  
CAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCTTGCTACCAGAGTGTG  
CTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCTGGAAAAGCTTCAGGGG  
ACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGAACTACCGAGCCCTTCAG  
CCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGATCCTCGTATACCACAGGT  
GAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTAT  
TTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCA  
GCACAAGCCACGACTGAGGCATAAATTCCCTTCTCAGATACCATGGATGTGGATGACTTCCCTT  
CATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTGGCCAGAAACACTGTAGGAGTAG  
TAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAGGAATGGACCCAGGCTGTCATTCC  
AGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAGGAAATCGCTGTG  
TTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGGGAAGTTTGGGATATACCCCAAAGTC  
CTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATATACTGCGGGATCTCTCCTTAGGATAA  
AGAGTTGCTGTTGAAGTTGTATATTTTTGATCAATATATTTGGAAATTAAAGTTTCTGACTTT

**FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPA SYPECGNNAQSPIDIQTDSVTFD PDLPA  
LQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQIN  
SEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQ  
KTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLESTE  
EEPSKLLVQNYRALQPLNQRMVFASFQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKI  
RKKRLENRKSVVFTSAQATTEA

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

**FIGURE 75**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGTG  
 TCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**CC  
 TACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTCA  
 TCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTG  
 ACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATAC  
 TCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGT  
 GTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTG  
 GAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACT  
 TTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCT  
 ATTACCGTGTTCCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAA  
 GAGAAACACCCAGCAAATTTGATTTTGTATTTATGGAAATGAATTTGACAAAAGATTCTTTGTG  
 CCTGCTGAAAAAATCGTGATTAACCTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCT  
 CATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCC  
 AGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCAT  
 TTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCCAGCAAGAG  
 TCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACC  
 ACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAA  
 GGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCACAAACGTTACAGTACTCA  
 TACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGG  
 CCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATT  
 CCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTC  
 GGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAA  
 AATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGATGGAAAAC**TGA**  
 TGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCA  
 GCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGTCTGTGAGAATTACTT  
 ATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTAGGTCTCTTAACAA  
 TGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAAAGCAGTCAATA  
 AATGTTTGCCAGACTGGGTGCAGAATTTATTTCAGGTGGGTGT

**FIGURE 76**

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQ  
IYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCA  
RTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILIIYGNEFDKRF  
FVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYA  
SHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVRTTDICAGPEEQELSLQEEVS  
TQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRL  
CIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEAPDRPPGENETYLMQFMEEWGLYVQMEN

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 77**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCGAGGTCTGGCATCCTGCACTTGCTGCCCTCTGAC  
ACCTGGGAAG**ATG**GCCGCCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTT  
GATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCCAAAAGTCATCAAAGAAAA  
GCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAG  
TGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCT  
GAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTC  
GGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCC  
CCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGA  
CACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCT  
GCGCATCCAAGTGTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGCAGGTCATGAA  
CCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTC  
CTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGA  
CCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGG  
GGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCT  
GACAATGCCCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGC  
TGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCTGTTGGACTCTGTGCTTCCCTGA  
GAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAGGCTGCAGATAAGCTGGG  
ATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTTATAGACCAAGGCCA  
TGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCAGTGAAGCCCTCCGCCCTTT  
GTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTACACCAAAGGTGACCAACTTAT  
ACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGATGAACTCTGGGATTGGCTGGTT  
CCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCACTCCATCCTGCTGCCGAACCA  
GAATGGCAAATTAAGATCTGGGGTCCCAGTGTCAATTGGTGAAGGCCTTGGGATTGAGGCAGC  
TGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTGGAAACCCAGCTC  
TCCTGTCTCCAG**TGA**AGACTTGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGT  
ATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCTGTGAAAAA

**FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAMR  
EKPAGGIPVLGSLVNTVLKHHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVK  
TIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLV  
PSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITIQLYLGA  
KLLDSQGKVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAABAVALSPEEFMVLLDSVLP  
SAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALR  
PLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL  
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLTTPASLWKPSSPVSQ

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

**FIGURE 79**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA  
 GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATGGC**  
 CTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT  
 TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCTGGTGCCAGCATTGTGACAGCAGT  
 TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA  
 CATCTATAGCACCCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGAC  
 ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTT  
 CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGG  
 AGGCCTCCTGGGATTTCATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC  
 ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTT  
 TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCCAGAGAAATCG  
 CTCCAACCTACTACGATGCCTACCAAGCCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG  
 TCAACCTCCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGTATGT**GTGA**AGAAC  
 CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCA  
 CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG  
 CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA  
 GGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCC  
 AACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGT  
 TTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTGACTGACCCTCTGTGATCAA  
 AGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT  
 GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC  
 TGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTG  
 AAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA  
 GGCAGCCTGGGACATTTAAAAAATA

1000  
 900  
 800  
 700  
 600  
 500  
 400  
 300  
 200  
 100  
 0

## **FIGURE 80**

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ  
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVFFI  
LGGLLGFIPIVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR  
NRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-24

#### **Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

#### **N-glycosylation site.**

amino acids 190-193

#### **PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59



**FIGURE 81**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTT  
 TCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTT  
 TCCTGCCCCACGCTGCTTCCTGGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGGGGT  
 CTGTGGGTTGATCTGTGGCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGACTCC  
 GCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGG**ATG**GTTCCCGAGGTGAGGGTCTCTCCTC  
 CTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACAT  
 GTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCC  
 ACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCG  
 CCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAA  
 GTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAAACGG  
 GACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAA  
 CCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCCGA  
 ACCAGGCTGCCCAGCACCCCTCCCCTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGC  
 AAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGA  
 TCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGCCCCCTGGCCTCAG  
 CGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACTGTCAA  
 GATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCCACGG  
 GGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTGCATCCTATGCACCTGTGA  
 GGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTACCCCCGA  
 GAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGACCCTGGCCACAGTGA  
 GATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTCGTCCACACATCGGTATCCCC  
 AAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACTTGGTGGAGATCTA  
 CCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAG  
 GCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGA  
 AAGAGGCACAGCACTTCGACTGCTCGCTGGCCCCCAGGAAGTCACTGGAACGTCTTCCTAG  
 CCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGAC  
**C****TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGC  
 ATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTC  
SEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIFSA  
HELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQ  
SLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKHKKAC  
VHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKCKICP  
EDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLR RFALEHEASDLVEIYLWKLVKDEETE  
AQRGEVPGPRPHSQNLPLDSDQESQEARLP ERGTALPTARWPPRRSLERLPSPDPGAEGHGQS  
RQSDQDITKT

**Signal peptide:**

amino acids 1-25

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCTCCGCTCACGCAGA  
GCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCC  
GTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTC  
TCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGC  
CAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTCTCCTA  
AGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGGTCCACC  
TCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGGACAAAAC  
TGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGA AACATTACTGTGTTGG  
ATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCATCTGGGAGC  
TACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGGATATGTTGATAGAGACA  
TCCAGCTACTCTGTCAGTCTCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAAGGTCCAC  
AAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGTATGTGG  
AGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATC  
TGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGAGCCTATATCGTGGC  
ACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTTGGCATTGTTGGACTGA  
AGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACTGGACTGGAGAAGAAAGCACG  
GACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGG  
CTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGG  
TGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAG  
GGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCGTGGGAGTGTGCCGGG  
ATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCA  
GACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGA  
CCCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAGTGTGGGACCATCTCCTTCTTCAACA  
TAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGTTTGAAGGCTTATTGAGGCCCTACA  
TTGAGTATCCGTCTTATAATGAGCAAAATGGAACCTCCATAGTCATCTGCCCAGTCACCCAGG  
AATCAGAGAAAGAGGCCTCTTGGCAAAGGGCTCTGCAATCCCAGAGACAAGCAACAGTGAGT  
CCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCA  
CATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCAGATCCAAAGTCCCGCAGCAGCCGGCCAA  
GGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCATGGCTGCCCT  
GAGCTGGGAGGGAAGAAGGCTGACATTACATTTAGTTTGCTCTCACTCCATCTGGCTAAGTGA  
TCTTGAAATACCACCTCTCAGGTGAAGAACCGTCAGGAATCCCATCTCACAGGCTGTGGTGT  
AGATTAAGTAGACAAGGAATGTGAATAATGCTTAGATCTTATTGATGACAGAGTGTATCCTAA  
TGTTTTGTTTCATTATATTACACTTTCAGTAAAAAAA

**FIGURE 84**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSV  
VHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAI  
WELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSRTNRDMHGLF  
DVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIV  
GLKIFFSKFQWKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAP  
QEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGHNRWRVGVCRDDVDRRKEYVTLSPDHGYW  
VLRLNGEHLTYFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLR  
PYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATTPFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255



**FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIIYPGPVVHGYWFR  
EGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGS I  
KWN YKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVSPLD  
PSTTRSSVLT LIPQPQDHGTS LTCQVT FPGASVT TNKTVHLNVSYP PQLTMTVFQGDGT VST  
VLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDA  
AEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRK KSA  
RPAAGVGD TGIEDANAVRGSASQGPLTEPWAEDSPDQPPPASARSSVGE GELQYASLSFQMV  
KPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGT  
ACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACA**ATGA**ACCAACTCAGCTTCCTGCTG  
TTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGG  
ACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGT  
GCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGAC  
ATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGG  
AAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGG  
GACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTAC  
AAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCCAATAAG  
TCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTC  
CAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGA  
AAGTGTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCCAGAAA  
ACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGG  
GTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAAC  
ACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGA  
GATTTTCTGGTTTTTGATTGGAGTGGATATGGAACCATGTTGGTTACAGCAGCAGCCGTGAG  
ATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGA**GAGTTTTGTGGGAGGGAACCCAGACCT  
CTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCAGTAGCTAGAATGTTAATG  
GCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAA

**FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENG  
VIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSA  
EAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGLIYQK  
YPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGGQREFTAGFVQFRVFNNERAANALCA  
GMRVTGCNTEHHCIGGGGYFPEAS PQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

**Important features:****Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298



**FIGURE 89**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAG  
ACCGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCT  
GACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACA  
GGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTACAGCTGGTGGC  
CGCGCTCTCTGTCACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTC  
CATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCT  
GTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCTTCTGCAG  
TGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAAGAAACC  
CTTCTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGT  
ATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCCTCGGAAACTGCTTCTGCTGGAGGA  
TATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAA  
TAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAA  
AAA

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGL  
FAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEM  
ALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0  
1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

**FIGURE 91**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACTG  
ACTCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGAT  
GATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGG  
GTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTA  
GGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAAC  
CACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAAC  
ATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACC  
TTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCC  
CCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCCTCCAA  
ATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTCGCTTTGCACC  
CACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCC  
CAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAG  
AAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCCTACTACCCATCTGGG**TGA**CCCCGG  
GCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGG  
ACACCGGGCAGGGAAGGGGTGGGCCTCAGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAA  
GTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAA  
GCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCTCTCTGTGCAGCCTCACA  
GGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCCTGTGGGCAGGCCGATCAG  
TGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGTTCTTGCCATCCTGAGGAAAG  
ATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTGTCAACTTAGGATGGATGGCT  
GAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGCCAGAGGAGCTCTCCAGCCCTG  
CCTAGTGGGCGCCCTGAGCCCCCTTGTCGTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACC  
CTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGCCAGGCCACCCCTTTCCAAA  
ATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATGGCACACCCATCCTTAAG  
CTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCCACAGCCCATCCGCGTGCTGTGTGTC  
CCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCGGAGAGGGGTCCCT  
CAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCCCGGATCTGGATGGCGCCGCCCTCTCAG  
CAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGAGCATGTGCTGGATCTGTTCTGTGTGTCT  
GTCTGTGGGTGGGGGGAGGGGAGGGAAGTCTGTGAAACCGCTGATTGCTGACTTTTGTGTGA  
AGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

## **FIGURE 92**

MLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANS  
TLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHG  
NGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTS  
LCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-14

#### **N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

#### **2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 93**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCG  
CCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTT  
TCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTG  
ACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATA  
TCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGA  
GTATAAACCCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCT  
TTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCA  
CAGTGGGCATTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCA  
TTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTTGATGGCTGTGAGAAGAAAAAGTGGG  
GCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTT  
ATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCT  
TAGCTGCGGGAGGCAGCTGCCGAAGCCTGAACTCTGCCTGCTCTGCCAAGACAAGAACTTTC  
TTCTTTACAACCAGCGCTCCAGATAACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACA  
TCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAA  
GAAATAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNK  
DGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGI  
MSGVFSFVNTLSDSLPGPTVGIHGDSPOFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKWGIL  
LIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSLKLCCLLCQDKNFLLY  
NQRSR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

#### **Glycosaminoglycan attachment site.**

amino acids 120-123

#### **Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 95**

[illegible]

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

### **Signal peptide:**

amino acids 1-16

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0  
1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0  
1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0



**FIGURE 97**

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCT  
 CTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCCTGAC  
**CATGGT**CCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGCCCA  
 GCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAACCTATGGTGAAATTTCCCTTTATACCTGAC  
 CAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCAGGCAA  
 GGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAGGGCCCT  
 GGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCAACCCTGGAGATGCAGGATGGACATGT  
 CTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTT  
 CTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCCCTTCCTCTT  
 CCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACCTCGGATCTTCGATTCCACATCCT  
 GAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCT  
 GGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTT  
 GGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAAGT  
 CTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGT  
 CCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGTGCACTATCACCTGGA  
 GAGCCATCCCCCGGGACCCCTTTGAAGTGAATGCAGAGGGAAACCTCTACGTGACCAGAGAGCT  
 GGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAGAATTTCCATGGCGAGGA  
 CTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAATGACAACGTGCCTATCTG  
 CCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCACCAGGTACTGAAGTGACTAG  
 ACTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCCCACGTTGTGTATCAGCTCCT  
 GAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCAGGTGGACCCCACTTCAGGCAG  
 TGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACATCCTGCTTCTGGTGCTGGCCAT  
 GGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAGTCGAAGTCGCAGTCACAGA  
 TATCAATGATCACGCCCCTGAGTTCATCACTTCCCAGATTGGGCCTATAAGCCTCCCTGAGGA  
 TGTGGAGCCCGGGACTCTGGTGCCATGCTAACAGCCATTGATGCTGACCTCGAGCCCGCCTT  
 CCGCCTCATGGATTTTGGCATTGAGAGGGGAGACACAGAAGGGACTTTTGGCCTGGATTGGGA  
 GCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAGGCAGCTCCAAG  
 TCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCCAGGCCCTGG  
 AGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGATGCCACCCCCCAAGTTGGACCAGGA  
 GAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTTCCTGCTGACCATCCAGCC  
 CTCCGACCCCATCAGCCGAACCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCTCTG  
 CATTGAGAAATTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGGA  
 CACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCCCTGTGCCCTCCCA  
 ATACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGA  
 TCTGGCCAGTGGGCACGGTCCCTACAGCTTCAACCCTTGGTCCCAACCCACAGGTGCAACGGGA  
 TTGGCGCCTCCAGACTCTCAATGGTTCCCATGCCTACCTACCTTGGCCCTGCATTGGGTGGA  
 GCCACGTGAACACATAATCCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGT  
 TCGAGTGATCGTGTGTCGCTGCAACGTGGAGGGGAGTGATGCGCAAGGTGGGCGCATGAA  
 GGGCATGCCACGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAAT  
 CTTCTCATCCTCATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGC  
 AGACAGCGTGCCCCCTGAAGGCGACTGT**CTGA**ATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGC  
 CTCTGGCTCCATCTGAGTCCCCTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGA  
 CAGAGTAGAAGCCCCTCCATCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCT  
 GCAGAGCCTGGACACCAACTTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTTTG  
 CCCAATAATAAAGCCCCAGAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAG

**FIGURE 98**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGK  
ATEGPFAMDPDSGFLLVTRALDREEQA EYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHF  
SQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFQLEPRLGAL  
ALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSIIESTWVSLEPIHLAENLKV  
LYPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQA EYLLQVRAQNSHGED  
YAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLL  
SPEPEDGVEGRAFOVDPTSGSVTLGVLPRLRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTD  
INDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTEGTFGLDWE  
PDSGHVRLRLCKNLSYEAPSHEVVVVQSVAKLVGPGPGPGATATVTVLVERVMPPPKLDQE  
SYEASVPISAPAGSFLTTIQPSDPISRTLRFSLVNDSEGWLCEKFSGEVHTAQSLQGAQPGD  
TYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRD  
WRLQTLNGSHAYLTLALHWVEPREHII PVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMK  
GMPTKLSAVGILVGTLVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 99**

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCC  
 TGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCC  
 TTTATCTCTTCACCTTCAAGTCCCCCTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCT  
 TGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAG**ATGA**AAGATGCAGAA  
 AGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGA  
 GACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAA  
 CTCTGGGTCCAGTGTGACCTCCAGTGGGGTCCAGCACAGCCACCATCTCAGGGTCCAGCGTGAC  
 CTCCAATGGGGTCCAGCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCAC  
 AGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTC  
 CAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGG  
 GGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAA  
 CTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACT  
 CTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCAC  
 AGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTC  
 CAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG  
 GGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGGGCTGGCACAGCCACCAA  
 CTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAGT  
 GTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCAC  
 AGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTC  
 CAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGG  
 GATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCCAGTGGGGCCAAACACAGCCACCAA  
 CTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACACAGCCACCAACTCTGAGTCCAGCACAGT  
 GTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGTCCAGCAC  
 AGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTC  
 CAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG  
 GATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCAAACACAGCCACCAA  
 CTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGAATGCACACAAC  
 TTCCCATAGTGCATCTACTGCAGTGAAGGCAAGCCTGGTGGGTCCCTGGTGGCGTGGGA  
 AATCTTCCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGCTCTTCTT  
 CTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCCTCATGG  
 CCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAGGTG  
 GAGTCCTAACTGGTTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGAA  
 CAGCGGGCCC**TGA**GCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGC  
 ACCCAAGACCTGGTTTCCTTTTCATTCATCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCT  
 GAAAATCTTGAAGAAGGTATTCCTCACCTTTCTTGCCTTTACCAGACACTGGAAAGAGAATAC  
 TATATTGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCT  
 GTGCTTGCCCCGGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAACCTCCAT  
 GCTGGACTCCATCTGGCATTCAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAA  
 AA

**FIGURE 100**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATIS  
GSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESS  
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS  
SGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGA  
GTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTA  
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNS  
ESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESS  
TVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS  
LVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP  
HRPRWSPNWFWRPVS SIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 101**

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCC  
TACGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACA  
GGTGGGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA  
ACAAATGGATGATGTGATAT**ATG**CATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT  
GGTCAATTAACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT  
TTGGAATCATGGTGTCATGGAAAGGGATTTACTTTATACTGACTCTGTTTTGGGGAAGCTTTT  
TTGGAAGCATTTTTCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATC  
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCCCTACCTGTGGCATTATTGGAGACCA  
TGTTTGGTGTAAGAGTGATTATAACTGGGGATGCATTTGTTCCCTGGAGAAAGAAGTGTCATTA  
TCATGAACCATCGGACAAGAATGGACTGGATGTTCCCTGTGGAATTGCCTGATGCGATATAGCT  
ACCTCAGATTGGAGAAAATTTGCCCTCAAAGCGAGTCTCAAAGGTGTTCCCTGGATTTGGTTGGG  
CCATGCAGGCTGCTGCCTATATCTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTCG  
AAGACATGATTGATTACTTTTGTGATATTCACGAACCACTTCAACTCCTCATATTCCCAGAAG  
GGACTGATCTCACAGAAAACAGCAAGTCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTC  
AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA  
GAGAAGGTAAGAACCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACAACATTCCTC  
AATCAGAGAAGCACCTCCTCCAAGGAGACTTTCCAGGGAAATCCACTTTCACGTCCACCGGT  
ATCCAATAGACACCCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGGG  
AAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAGGGGAGAAGAATTTTTATTTTACCGGAC  
AGAGTGTCATTCCACCTTGCAAGTCTGAACTCAGGGTCCTTGTGGTCAAATTGCTCTCTATAC  
TGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTTAAGT  
GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA  
TCATAGAACTTGCAATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG  
AG**TAA**GATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTGGAAATGTTCTAAACCTT  
TCTAAGCTCAGATGCATTTTTGCATGACTATGTGCAATATTTCTTACTGCCATCATTATTTGT  
TAAAGATATTTTGCACCTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTAATCTCTGAA  
TGTAATTTTCGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTTGGGCCAGAATA  
TTATTAAACAATCATCAGGCTTTTAAA

**FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSF~~GIMVSWKGIYFILTLFWGSFFGSIFML~~  
SPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMF~~GVKVIITGDAFVPGERSVIIMNHRTR~~  
MDWMFLWNCLMRYSLRLEKICLKASLKGVP~~PGFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYF~~  
CDIHEPLQLLIFPEGTDLTENSKSRSNAFAEK~~NGLQKYEYVLHPRTTGFTFVVDRLREGKNLD~~  
AVHDITVAYPHNIPQSEKHL~~LQGDFPREIH~~FHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERL~~~~  
RSFYQGEKNFYFTGQSVIPPCKSEL~~RVLVVKLLSILYWTLEFSPAMCLLIYLYSLVKWYFIITI~~  
VIFVLQERIFGGLEIIE~~LACYRLLHKQPHLNSKKNE~~

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

**FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGA  
 CCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACAGG  
 AATATCC**ATG**GCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTG  
 GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG  
 CTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGTTCTTCAGGAATCAGTTCCA  
 TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG  
 AGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAAA  
 CATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAAGTTCCAGATTACGATGAGGA  
 GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATA  
 TGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCCCCAGCCACAGCCAA  
 GTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAG  
 CCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCAT  
 CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA  
 GCCCTCACCTTGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGT  
 TGTGATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTG  
 GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCT  
 GGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTGAACCCATAGAAA  
 AGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA  
 GGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT  
 GGGAGTGTGTCGGGATGACGTAGACAGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGG  
 GTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTACATTCAATCCCCATTTTATCAG  
 CCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCTGGACTATGAGGGTGGGACCAT  
 CTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCTGCTGACATGTCAGTTTGAAGG  
 CTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTTCAT  
 ATGTCCAGTGTCTTGGGGAT**TGA**GACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACAGACC  
 CAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCTCCGGAGCCTGCGC  
 ACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA  
 GCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAGTCAGAAGCC  
 ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAACCTCCATC  
 CAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGGACAGT  
 GATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTTTGA  
 GGGCACAGTGTGTTGCTAATGATGTGTTTTTATATTATACATTTTCCCACCATAAACTCTGTTT  
 GCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC  
 CTGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTCACTGATTCTATAAGCCCAG  
 CATTACCTGATACCAAACAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCA  
 TATCCCTCATTAACACAGACACAAAATTCTAAATAAAATTTTAACAAATTAACTAAACAAT  
 ATATTTAAAGATGATATATAACTACTCAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAA  
 TATTTAAATATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAA  
 AAAAAAAAAA

**FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV  
VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT  
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLY  
DVEISIIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVM  
GMIIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAP  
QEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDGRKNNVTLSPNNGYW  
VLRLTTEHLYFTFNPFIISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLL  
RPYIQHAMYDEEKGTPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259



**FIGURE 105**

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTAG  
 GAAAAGAGTTTGTGGGAACCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCT  
 GGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATTA  
 CTATAGCACATTGTCATTTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAA  
 CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC  
 ATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGGAGTGTT  
 GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAACTGTAGATAAAAT  
 TGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAGATCCTCA  
 CTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG  
 AACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGA  
 GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTT  
 AATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAG  
 ATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAAT  
 AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGCAGAGCTTTC  
 TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT  
 TCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAATGATGGTTACAGTCA  
 AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTTGCAATGAACCTCAAGC  
 TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC  
 ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGC  
 TGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTTTATACTAGAGT  
 TACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATC**TAAG**AGACAAAAGCCTCATGGAA  
 CAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGA  
 AGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAACTGTTTGCTTGATGCATGTATTTT  
 CTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA  
 GCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAAATACAATATTACATTACAGCCTGTA  
 TTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAAGTTGTTGACATAAATTTGTAATGCATA  
 TATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAATATCCA  
 TTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCTACATTTTA  
 TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTCATTAT  
 GAAAGGTCAAGCAAAGACAGCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACATA  
 GTTAAGGAAGTCCAGAAAGAAGCCAAGATATATCCTTATTTTCATTTCCAAACAACCTACTATG  
 ATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCTATAATAATTATACAACTTCATGCAATG  
 TACTTGTTCTAAGCAAATTAAGCAAATATTTATTTAACATTGTTACTGAGGATGTCAACATA  
 TAACAATAAAATATAAATCACCCA

**FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTDK  
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFH  
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS  
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIK  
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDVMFVTG  
FGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGPLV  
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

**FIGURE 107**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCC  
 TGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC GGCC  
 CAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTC  
 TCCCTTACGGGGCTCACA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTAC  
 GCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGG  
 GACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTG  
 ACTTACTTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTTGTGGGG  
 ATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGT  
 TTGCTTGTCAATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTTATG  
 GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCT  
 AGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAGTGCTGTGGAGTA  
 GTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCCCTGCTGTGTT  
 AGAGAATTTCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG  
 GGTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAAACAACCTGCAGGTGCTGAGGTTT  
 CTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGG  
 GCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAAC  
 TCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAA  
 CACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTA**TAAA**AAGAAATG  
 TCACAGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTG  
 TTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA  
 TGCTTTAAAATGAGGATGGAAAAGTTTCATGTCAAGTCAACACCTGGACAATAATTGATGC  
 CCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAAC  
 ACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACA  
 TATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACT  
 AATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTC  
 TTCTGATGCTAAATAAATTATATATCAGAAAACCTTTCAATATTGGTGACTACCTAAATGTGAT  
 TTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCT  
 GATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTTCAGTTCT  
 GATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTTA  
 GCCTTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAACTGTTA  
 TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGA  
 ATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAA  
 AGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTTGACACTAAACACTTTTTTAAAA  
 AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGA  
 AAATAGTGTTCTTTTTCTCCAGAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAG  
 AGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTT  
 TTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTAT  
 TTTGTTTATTTCTCAGAATATGGAAAGAAAATTAAATGTGTCAATAAATATTTTCTAGAGAG  
 TAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV  
HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS  
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTENDWPPDSCCVREFPGC  
SKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR  
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

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**FIGURE 109**

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCC  
 CTACCAAGTGCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGA  
 AAGAGAAGGGGACAAAGGAACACCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTC  
 CAGAAGG**ATG**CCTCCATTCTGCTTCTCACCTGCCTCTTCATCACAGGCACCTCCGTGTCACC  
 CGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA  
 CCAGTTGGATGAGTCTCAAGGTCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA  
 CTTACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAAC  
 CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCA  
 GGCTTGTGCCAGCTTCAATGGGAACTGCTGTCTCTGGAACACCACGGTGGAAGTCAAGGCTTG  
 CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGG  
 TCATTTTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATACCAGCGAGTGCAC  
 ATGCGCTCCAGGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTGATGAAAATGAATGTGA  
 GCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAACTCCTACCGCTGTGAGTG  
 TGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA  
 TAACAATGGTGGCTGCAGCCACTCTTGCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCC  
 CCGGGGCTTGGTGTGTCTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAA  
 TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTTGGTGGCCTGGAGCTCTTCCTGACCAACAC  
 CTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACATCCTCTTCTCTCAAGACATGTGG  
 TACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA  
 GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTGAC  
 CTGCGAGTTTCCACGCCTGTACACCATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCC  
 ACTGGAAATCATGAGCCGAAATCATGGGATCTTCCATTCACTCTGGAGATCTTCAAGGACAA  
 TGAGTTTGAAGAGCCTTACCGGGAAGCTCTGCCCACCCTCAAGCTTCGTGACTCCCTCTACTT  
 TGGCATTGAGCCCGTGGTGCACGTGAGCGGCTTGGAAGCTTGGTGGAGAGCTGCTTTGCCAC  
 CCCCACCTCCAAGATCGACGAGGTCCTGAAATACTACCTCATCCGGGATGGCTGTGTTTCAGA  
 TGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGGTCCCTGTCTT  
 CAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTTCTGCACTGCCGGGTCTTGTCTGTGGAGT  
 GTTGGACGAGCGTTCCCGCTGTGCCCAGGGTTGCCACCGGCGAATGCGTCGTGGGGCAGGAGG  
 AGAGGACTCAGCCGGTCTACAGGGCCAGACGCTAACAGGCGGCCCGATCCGCATCGACTGGGA  
 GGACT**TAG**TTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTC  
 CCCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTTCAGACTTCACACTGTGAGTTCAG  
 ACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCACAGGTACACAGCACTGCTG  
 AACAATGTGGCCTGGGTGGGGTTTCATCTTCTAGGGTTGAAAATAAATGTCCACCCAGAA  
 AGACACTCACCCCATTTCCCTCATTTCTTCTTCTACACTTAAATACCTCGTGTATGGTGCATC  
 AGACCACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAG  
 TTAAGTAAATTATGACTTAAATACCAATGACTCCTTAAATATGTAAATTATAGTTATACCTT  
 GAAATTTCAATTCAAATGCAGACTAATTATAGGAATTTGGAAGTGTATCAATAAAACAGTAT  
 ATAATTTT

**FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFT  
 GMAGDAMPTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPG  
 GYYVYRLTKPSVCFHVYCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQN  
 NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDVEGCHNNNGGCSHSCLGSEKGYQCECPRG  
 LVLSEDNHTCQVPVLCKSNAIEVNIPRELVGGLLEFLTNTSCRGVSNNGTHVNILFSLKTCGTV  
 VDVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE  
 IMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLRLDSLYFGIEPVVHVSGLESLVESCFATPT  
 SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRVLVCGVLD  
 ERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPPIRIDWED

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
 522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

**FIGURE 111**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT  
GCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC  
TGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC  
GGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG  
ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCA  
TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATTC  
TGGATAAATACTACTTCTCCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTG  
ACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG  
GGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCA  
CAGGGAAGTGGTTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAGACAGCCTGTA  
GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAA  
TCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCTCTCAGGCTCCC  
TGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGG  
AGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGACAAACAGCACGTCT  
GTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATA  
CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCATCCCTGG  
CTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCC  
TCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT  
TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGA  
ATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGT  
GCAATGCAGACGATGCGTACCAGGGGGGAAGTACCCGAGAAGATGATGTGTGCAGGCATCCCGG  
AAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGGCCCTGATGTACCAATCTGACCAGT  
GGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCAGGAGTAT  
ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG**TAAT**GCT  
GCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCCAA  
AGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTT  
GGAGCAGCAAAGGGCCTCAATTCCCTGTAAGAGACCCTCGCAGCCCAGAGGCGCCCAGAGGAAG  
TCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACT  
GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGC  
AGGCTGTCTTGTAAGAGCCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCA  
GCCCTGTCCGTCTTACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAAT  
GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGG  
CCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAA

**FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL  
CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA  
CFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPGCLSGSLVSLHCL  
ACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWK  
VRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTP  
ATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCTC  
QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)



**FIGURE 113**

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT  
 TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCACAG  
 GAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT  
 AAAATCTGTTTTTTGTTCTCTTGTAACCTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACT  
 GTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT  
 CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC  
 TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTAGCTGCGG  
 CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGAACAAGCCCGAAGATTTATAGGCG  
 ATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG  
 GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCATCTAACCTTTT  
 CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCT  
 TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA  
 CTTGCATTCTCCTGGAACATGAGGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG  
 TGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTATCACAAGGCATCGAGTCTCCTGC  
 ATTCAGTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG  
 GGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC  
 CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG  
 GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT  
 CCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTTGGCCCAGGA  
 GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT  
 AAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT  
 AATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT  
 TATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA  
 TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG  
 GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC  
 TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG  
 AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT  
 TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTATGGTTATTT  
 GTAA

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## **FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS  
PCWPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15

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**FIGURE 115**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGGC**  
AAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA  
GAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAAT  
TGTCTGTGTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA  
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAG  
AACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA  
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGT  
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTT  
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA  
AAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAAT  
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGA  
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG  
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGA  
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTA  
TTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG  
ACGAGTCATCTGTCGTGTCATCATGCCTTGTAACCTGGTGGGTGGCCCGCATGCTGGGGAGGGT  
**CTAA**TAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATATAATAAATGCATGCTATT  
CAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG  
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 116**

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPPKKAYD  
 MEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQI  
 KVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWINPT  
 LISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG  
 IEFDPMLDERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWWVARMLGRV

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

### FIGURE 117

GAGCTCCCCTCAGGAGCGCGTTAGCTTACACACCTTCGGGACAGGAGGGCGGCAGCTTCTCGC  
AGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCTCTCC  
TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGG  
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA  
GGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCACATCCTGGGACTTCCAGCCATGC  
TGCAGGCAGTGCAGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT  
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGA  
CACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT  
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG  
GGATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTGGGCTGGGTCTG  
CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAG  
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTGCCTACAAGCCTG  
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAAACAAGAAGATATACGATGGAG  
GTGCCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGTG**TAA**TGCTCTA  
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCCA  
TCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCATCTTTG  
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG  
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTTAAATATAA  
CTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAG  
ACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAG  
AAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTC  
CCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATT  
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCA  
AAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC  
AACACCATTCTAGGAGTTTCCTGAGCTCTCCACTGGAGTCCTCTTTCTGTGCGGGGTCAGAAA  
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTAAAGTCCTAAATATAGTTAAAATAA  
ATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG  
AAGGAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA  
GTACAAATTTCCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG  
ATCACTTGAGCCCAGAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA  
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAG  
GCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC  
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAAATAAAAAATAAATAATGGA  
ACACAGCAAGTCCTAGGAAGTAGGTTAAAACATAATTCTTTAA

## **FIGURE 118**

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTEC  
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFI  
VSGLCIAIGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG  
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ  
SYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

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**FIGURE 119**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG  
 AGTCCAGCTGGCTAAAACTCATCCCAGAGGATA**ATG**GCAACCCATGCCTTAGAAATCGCTGGG  
 CTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA  
 GTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTGGATG  
 AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT  
 TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCT  
 TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG  
 GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGTCTATCCCT  
 GTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA  
 AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGA  
 GGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA  
 CCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC  
 AGAAGTCAGTATGT**TAG**TTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATGACA  
 AAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGC  
 CTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGCAGAA  
 TGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG  
 TTCAAGCATCTACTCTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT  
 ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCA  
 CATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT  
 AGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTG  
 TTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAAATGAAGGCTTTAA  
 TCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAA  
 ATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT  
 TTTAAACGCAGATATTTTGTCAAGGGGCTTTCATTCAAACCTGCTTTTCCAGGGCTATACTC  
 AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAAAATATTTTT  
 GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT  
 TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT  
 GTCTTGGTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTC  
 ACCTGCTCCTATGTGGGTACCTGAGTCAAATTTGTCATTTTTGTTCTGTGAAAAATAAATTC  
 CTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT  
 CCAATTTGATGAACTGACAATCCAATTTGAAAGTTTGTGTGACGTCTGTCTAGCTTAAAT  
 GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNI VVFENFW EGLWMNCVRQANIRMQ  
CKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF  
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN  
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

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**FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG  
AGCCAGACGCTGACCACGTTTCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGC  
AGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGC  
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA  
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG  
CAGGAGTGCCTGGTTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC  
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT  
GGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA  
TTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCT  
CACTTCGGCTAAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTG  
AATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA  
ATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG  
GATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA  
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TAA**ATGCTTTAATTTT  
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAG  
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCA  
CACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGTGGTTTCAATATTTTTTTT  
TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG  
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG  
TACAATTTGTAAATGTAAAGAATTTTTTTTTATATCTGTTAAATAAAAATTATTTCCAACA

## **FIGURE 122**

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAAGVP  
GRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC  
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTI  
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 195-217

## FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTG  
AACTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC  
CCAAATTGCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTT  
TTTTTAACCGCCCCCTCCCCACCCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCAT  
GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTT  
GTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG  
GGGTCCAATTTTTCTTCTGGGTGTGACGAGCCCTGACTCACTACAGTGCAGCTGACAGGGG  
CTGTCATGCAACTGGCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAA  
AGG**ATG**GGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCC  
ACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGGCTGTAGGTGTGAA  
GGCAAAATGGTATATTGTAATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGT  
TGCTTAGGTTTGTCCTTCGCTATAACAGCCTTCAAAACTTAAGTATAATCAATTTAAAGGG  
CTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT  
TTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTT  
AACAAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCTTATAATCAGCTGCAT  
TCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTTACATTTACGGTCTAAC  
TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAACCTTTGGACCTG  
GGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGCATGATCAGACTCAAAGAA  
CTTCACCTGGAGCACAAATCAATTTTTCCAAGCTCAACCTGGCCCTTTTTCCAAGGTTGGTCAGC  
CTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTCATAGGACAGACCATGTCCTGGACC  
TGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT  
GTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAAGCTCACATTTATT  
GGTCAAGAGATTTTGGATTCTTGGAATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG  
GAATGCAGCAGAAATATTTGCTCCCTTGTAAACTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG  
AATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG  
AACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAGGGCTCTCCCAAAG  
CCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCCCTTTGCCCCCGACG  
GTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCTTCCATAAA  
ATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTATCTACGTG  
TCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAAGGCAC  
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTTATGTAGAT  
TATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCTGCACCTAT  
AACAAATCGGGCTCCAGGGAGTGTGAGGTA**TGA**ACCATTGTGATAAAAAGAGCTCTTAAAGC  
TGGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTC  
CCCTTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTCATA  
ATACTGGTCATTTTCTCTCATAATAATCAACCCATTGAAATTTAAATACCACAATCAATGT  
GAAGCTTGAACCTCCGGTTTTAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAAT  
GTCGCATTTGTTTTAAGATAAAACTTCTTTCATAGGTAAAAA

**FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGC  
 LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLN  
 NTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELLDLG  
 YNRIRSLARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLYLQWNKISVIGQTMSWTW  
 SSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLAGNIWE  
 CSRNICSLVNWLKSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLARALPKP  
 TFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKI IAGSVALFLSVLVILLVIYVS  
 WKRYPASMKQLQQRSLMRRHRKKKRQSLKQMT PSTQEFYVDYKPTNTETSEMLLNGTGPCTYN  
 KSGSRECEV

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 125**

CCGTTATCGTCTTGCGCTACTGCTGA**ATG**TCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGC  
TGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCG  
AGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTC  
TTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCC  
TAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACA  
GACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTG  
GCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTG  
TTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTTCAAGATGCAAATGGAAGGAA  
AAAGGAACTGGAAGGAAAACCATTCGCGATTTCGTGGTGTACATCATGCATTTGCAAAAATCT  
TAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCAC  
TGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGTATTGAATACAC  
CACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTA  
TTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCACGAGATAAACAAG  
GAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAGGCTGTTCAAGGTGAAGGAT  
TCATGAGTCTATATAAAGGCTTTTTTACCATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGT  
TCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCATTT**TAA**

**FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGAR  
ESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYP  
LWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFKILAEGGIRGL  
WAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVI  
KSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFGMSLYKGFLPSWLRMTPWSMVFWLTYEKIR  
EMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

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**FIGURE 127**

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCG  
ACCCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCC**ATG**GCCAGGCCCGGC  
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGGCCTCGGGGGGCATCGGCGCGGCC  
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC  
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCTACAGA  
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC  
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCTGACACCCTGCTCTCAGGCAGC  
ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA  
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATG  
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC  
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACG  
TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCTTCAAACCTCCACGACAAGGACCCTGAG  
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT  
ATCTACGTCCTCAGCACCCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCCACGGAG  
CAGGTGACCT**TAG**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCTCCTG  
CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATACCACTTCCTGTCCACACCCCGACC  
AGGGGCTAGAAAATTTGTTTGAGATTTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG  
TGAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTCTTG  
TGCCCTGGGCACCTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT  
GTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG  
GAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC  
ACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCCAGTCTTGGCTTCTTGT  
CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC  
CCAGTGGATTTTCATGGTGATCATTAAGAAAGAAATCGCAACCAAAAAAAAAAAAA

**FIGURE 128**

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGT  
LIPYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFN VNVLALS  
ICTREAYQSMKERNVDDGHIININSMSGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT  
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ  
MRPTEQVT

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114



**FIGURE 129**

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC  
ATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAAGTGCAGAGTCTCAGTTGCCCCG  
GAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCAGAAATCCAGTTCTGGTT  
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTT  
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAG  
CCACCTGTGGCCGTTGAGTGCTTGAAATGAGGAACTGAGAAAATTAATTTCTCATGTATTTTT  
CTCATTTATTTATTAATTTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGG  
ATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACAT  
TTATTTTTTTATTTCTTTTTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGTGCC  
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA  
GTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTTTTAGTAGAGACG  
GGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCTCG  
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTT  
CTTTGTGTTGGGAACCTTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG  
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT  
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC  
CATGAGATCCACTTTTTTTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG  
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAATGACAGGA  
TTTCGTTCTTAATTTCAATTAATAAACCACACATGGCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRI PVLVSCQ  
PVKGHGTLGESMPFVKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

**FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACC**ATG**ATCAGCGCAG  
 CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTCTATCAG  
 TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC  
 GCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACA  
 ACCAAATAAATAATGCTGGGATTCCTTCAGATTGAAAAACTTGCTGAAAGTAGAAAGAATAT  
 ACCTATACCACAACAGTTTAGATGAATTTCTTACCAACCTCCCAAAGTATGTAAAAGAGTTAC  
 ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTCCCTATCTGG  
 AAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTCGGAG  
 ACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAAATCCCTGGGGTT  
 TGCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCAT  
 CTCTTCAAGGTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATG  
 GTTTAGGTGACAAAGTTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT  
 CCCTGACTGCTGCACCAGTAAACCTTCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA  
 ACCACATCAATCGGGTGCCCCCAAATGCTTTTTCTTATCTAAGGCAGCTCTATCGACTGGATA  
 TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC  
 AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT  
 TACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTT  
 GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA  
 GCACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAG  
 CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG  
 GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCATA  
 TCTCTTGAAACTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATA  
 GCCCCGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA  
 CAGCCCTGGAGCCTGATTCACCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT  
 ACCTATTTGATGAAACTCCTGTTTTGTATTGAGACTGAACTGCACCCCTTCGAATGTACAACC  
 CTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAACCCCAATTTACCTTTGG  
 CTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGT  
 ATGTTCATAGGAATGGATCGCTCTTCTCAAGGAACTGTGCATATAGCAAAGGGAGGAGAAGAA  
 AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTT  
 CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAATACACACCA  
 TATTTCTCCTAATGGAATGAATCTGTACAAAACAATCACAGTGAAAGCAGTAGTAACCGAA  
 GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACTCA**TGA**TGCTGAAGGACTCACA  
 GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFTIYCNDRFLT SIPTGIPEDATTL  
 YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNI RTITYDSL SK  
 IPYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST  
 ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLT AAPVNLPGTNLRKL  
 YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDL DNITQLILRNNPWYCGCKMKW  
 VRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELFDC KDSGIVSTIQITTAIPNTVYPAQ  
 GQWPAPVTKQPDIKNPKLTKDQQTGSPSRKTITITVKS VTSDTIHISWKLALPMTALRLSWL  
 KLGHS PAFGSITETIVTGERSEYLVTALEPDSPYKVC MVPMETS NLYLFDETPVC IETETAPL  
 RMYNP TTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSK  
 GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGM NLYKNNHSES  
 SSNRSYRD SGIPDS DSHS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 531-552

#### **N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

#### **Tyrosine kinase phosphorylation site.**

amino acids 515-522

#### **N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
 640-645

#### **Amidation site.**

amino acids 567-570

#### **Leucine zipper pattern.**

amino acids 159-180

#### **Phospholipase A2 aspartic acid active site.**

amino acids 34-44

**FIGURE 133**

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGG  
 CAGCCCTGCCGGGCCACTTGTCTTC**ATG**TCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG  
 GGCGTGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA  
 GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC  
 GCTGTGGTCCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT  
 GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCT  
 GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGGAGAAGTGGGC  
 CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC  
 TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA  
 GCTGACCCTCCAGCCCCGGTTTTGGGAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTT  
 GGTGTACCCACGTTTCGGGCCCCAGGACTCATTTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT  
 GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG  
 CCTCATGACCAAGCCCCGGCTGCTCAGGCTACTGCCTGTCCCACCAACTGCTCTTCTTCTCTG  
 GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT  
 CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCTACCCG  
 GGACATCTTCATGGAAAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT  
 CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA  
 TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA  
 GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA  
 TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCCTCATCCTCCCGAG  
 TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTATATTTTTTTTAGTAGAGAC  
 AGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCACCTC  
 AGGCTCCCAAAGTGTTGGGATT**TAG**GTGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAAA  
 GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC  
 TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCCTATACA  
 TCCTGGCAGAATAACCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA  
 GCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCTCTCA  
 TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA  
 GCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG  
 AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

## **FIGURE 134**

MSARGRWEGGGRRACRGSGLLARAQGAERVTSSEQRPAMASLGLLLLLLLLLTALPPLWSSSLPG  
 LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL  
 SLRVGMLGEKLEAAIQRSYLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ  
 DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ  
 GPLQQSQDYINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS  
 WQKQQEGCFGEFDAEDEELSKAIQYQQHFSSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP  
 PGFKQFSCILLPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 39-56

#### **Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

#### **N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

#### **Amidation site.**

amino acids 10-14

#### **Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

**FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTC**ATG**GCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC  
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGG  
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG  
TGAAGCCTCAGGACTGGATCTCGGCGGCCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT  
TCCTTAAGACAGATGGGAGTTTTGTGGTTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG  
TTGTATCTCCAGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGA  
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA  
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTC  
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG  
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT  
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAATCATCTG  
GCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAAGGAGG**TAG**TCAG  
GCCGTCCAGAGCTGGCATTTCACAAAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAA  
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACTGTGTATGTT  
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT  
ATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCCATAGAAAATGCCATTAATAAA  
TTATATGAACTACTATACATTATGTATATTAATTAAAACATCTTAATCCAGAAATCAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

**FIGURE 136**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWIS  
AARVLVDGEEHVGFLKTDGSEFVVHDIPSGSYVVEVVSPAYRFDVVRVDITSKGKMRARYVNYI  
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPD  
MRREMEQSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

**Important features of the protein:****Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236



**FIGURE 137**

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTACGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCCTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAAAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG  
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTATTCAATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSELRPE  
IFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE  
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTPDHY  
TLRKISSLANSFLT IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI  
LLQWMEETE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 139**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTTCGGTTCGCATCCAG  
 CCTAGCGTGTCCACG**ATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAG  
 GTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTTCTCTGCCAGA  
 GCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCTCGGCTGGAGCCAGTTCTAACTGGACC  
 ACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGAT  
 TTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAAAAAGGA  
 GCATCTCACAGTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCA  
 TTGATGACGGGGAGCCTTCTCGGCTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTG  
 CTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGAT  
 GAAACCTGGGTAAATTATTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTTC  
 GTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGA  
 GGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGCCACATTTACGGG  
 CCAAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCAC  
 ACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGGTTCTTTGTGGTGAC  
 CATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAGGTGAATACACCTCTG  
 ATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACATCCAAAGCACGTCCAA  
**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGATTCCAAAAGACAGTGTA  
 GGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAGCAGTTGAGATTTTTTACAT  
 TTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCCGTATATGAAAAGATCCT  
 GGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGGGAACTGGATCAGACTGTACTTGGAG  
 GAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGGTTCTCAGGCAGTACCTGGATGCT  
 CTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAGTTCTCACCTGCTCCTGCTCA  
 GCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCACTGTATCTCCTGGGTTTT  
 CTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCGTTACGTCATTGTGTGCACCTCAG  
 CTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCTGCCTTTTCGTTTACCA  
 GACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCTGGACAGGGGGCCTCAGG  
 GAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGTGTCCCGACACAGGTGTTACATCTGT  
 GCTGTGAGGTGAGATGCCTCAGTTCTTGAAAGCTAGGTTCTGCGACTGTTACCAAGGTGAT  
 TGTAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAATCGGACA  
 GCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGACACTC  
 AGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCAGAATGCATCCTGCC  
 TCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTCTTAGTCCTTGGCCT  
 CGGACACCTTCATTGCTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCA  
 CACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCC  
 CCCACCCCAACCCTGCACAGCCCTCATCCCCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTG  
 AGTGTCTGACCGAGACACTCACAGCTTTGTATCAGGGCACAGGCTTCCTCGGAGCCAGGATG  
 ATCTGTGCCACGCTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATT  
 AGTACCTAGCTGCACACAGTATGTAGTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPP  
 LFSKVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGS  
 LPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVSDYT  
 EVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNPLIGQKLSEMDSVLMKIHTSLQS  
 KERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
 275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208

**FIGURE 141**

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTA  
CAGAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTG**ATG**TTACTGCTGCTGTTGGAGTAC  
AACTTCCCTATAGAAAACAAC TGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAAC  
TTAAACCCGAAGAAATTCAGCATT CATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGG  
AATCTCATAGCAGTTCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCA  
TCCTTGAGCTCAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAG  
TTTTGTCTCTACTGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAG  
AAACTGATGAAGCTGGCTGCCCAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCT  
CAGGTGGGCTCCTGGAACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCC  
TGCAATTGTAATGAGCCTGTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTT  
TCATTTCAACCAGTTTGCAAAGCTGAAATGAGCCCCAGTGAGGTCAGCGAT**TAG**GAAACTGCC  
CCATTGAACGCCTTCCTCGCTAATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

## **FIGURE 142**

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKEFSIHDQDHKVLVLDSGNLIAVDPKNIYIRP  
EIFFALASSLSSASAEKGSPIILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESAR  
RPFIFYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPS  
EVSD

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 33-36

**N-myristoylation site.**  
amino acids 50-55, 87-92

**Interleukin-1**  
amino acids 37-182

[illegible]

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSK  
DYYAYRLGHILNSWKEQVESKTVFSMELLLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTI  
STRPWMTQFSLLNKTCLGEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

144/168



**FIGURE 145**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCG**ATG**AGGA  
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG  
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCCAGCACTGCCC  
AGATCACTGAGGCCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGC  
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTA CTACGAGGCCAACTACTGGCAGTTCCCCG  
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT  
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC  
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG  
AGAGGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA  
TCTGGCTCATGGTGAAA**TAA**GCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA  
TCCTGGCAAGTGACCCAGCTCTTCTCCCCAAACCCACGCGTGTTCTGAAGGTGCCCAGGAGC  
GGCGATGCACTCGCACTGCAAATGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT  
GATAGATGGGGGACTGTGGCTTCTCCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA  
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC  
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTACAGATAAGGAAACTGAGGC  
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC  
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT  
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT  
TAGAAATAAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQG  
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK  
LHQQVLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMVK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 157-171

#### **N-glycosylation sites.**

amino acids 98-102, 110-114

#### **Tyrosine kinase phosphorylation site.**

amino acids 76-83

#### **N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

#### **Amidation site.**

amino acids 62-66

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT  
TTCCTGATGATTTATAGACTCAAAGAAAAC**TATG**TTCAGAAGCTCTCTTCTCTTCTGGCCTC  
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA  
AGCTGGAAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCACTGAGTCTTAGTTTTTATTTTT  
TGAAATTTCAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT**T**  
**GAT**GTCTGAGGTTTGGGGT

[illegible]

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT  
CEGLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

148/168

**FIGURE 149**

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGAC  
 TTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGC  
 CGCCAGTCCCGGCCCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTACTCC  
 TCCTTTTCATTATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCC  
 GAGCGTGGAAGA**ATG**GGGTTCTTCGGGACCGGCACCTTGGATTCTGGTGTTAGTGCTCCCGATT  
 CAAGCTTTCCCCAAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCA  
 GAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAACATATCCT  
 CCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTGATAACTTGAACCTGCTAAAGGCA  
 ATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCACTTGATAAT  
 AAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGATTATGACTCT  
 ACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATCAACTAGACGGG  
 ACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAGAAAATGAC  
 AGAGCCGTGTTTGACAAGATTGTTTCTAAACTACTTAATCTCGGCCTTATCACAGAAAGCCAA  
 GCACATACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAAC  
 AATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCA  
 GAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACA  
 GTATCTAACACATTAACTTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGAC  
 AACTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAA  
 AAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAG  
 ATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTTCCTACCTTGAAAACCTGGAT  
 GAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAATGCTACTGACAATATAAGCAAG  
 CTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAAGCAGCT  
 AAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAAGATGATAACTCCAACCCAGGA  
 GGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGCCATCAGAAAAAATATT  
 GAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTTCAAAGATGAGA  
 GACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAAGAAGCC  
 GAGGCCATCAAGCGCATTTATAGCAGCCTG**TAA**AAATGGCAAAAGATCCAGGAGTCTTTCAAC  
 TGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAAATTTTTTGACCC  
 AAGGGTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGC  
 TTTCTTCCCGTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAA  
 AAA

**FIGURE 150**

MGFLGTGTWILVVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENK  
PGQSNYSFVDNLNLLKAITEKEKIEKERQ SIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSG  
LDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTL  
EDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGK IPEKVTPMAAIQDGLAKGENDETVSNT  
LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVK  
YGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEEAAKMEK  
EYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFIN  
KQADAYVEKGILDKEEAEAIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

**FIGURE 151**

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTC  
 AAG**ATG**GTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTAT  
 CTGCATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAG  
 ATCAGCGTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAG  
 GGTGGAAGCCAGTGCCTGTCTGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTG  
 AACATCATGGAGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGAC  
 ATGGGGCTCACCTCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCT  
 GAAGCCGATCAGCCTGTCAGACTCACCCAGCTTCCCAGAAATGGTGGCTGGAATGCCCCCATC  
 ACAGACTTCTACTTCCAGCAGTGTGACT**TAG**GGCAACGTGCCCCCAGAACTCCCTGGGCAGAG  
 CCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAG  
 GACCCCCACGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGGATAA  
 ATTCTGAGATTTGGAGCTCAGTCCACGGTCCTCCCCACTGGATGGTGTCTACTGCTGTGGAAC  
 CTTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTG  
 GGGGAGTGGTGGGAATCATTCCTGCTTAATGGTAACTGACAAGTGTTACCCTGAGCCCCGCAG  
 GCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTCCTGTCACTC  
 ACCACTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCTTGCCCCAGCCCC  
 ACCCCCTTCCCTTTAATCCTGCCACTGTCTATGTACCTTTCCTATCTCTTCCCTCATCATC  
 TTGTTGTGGGCATGAGGAGGTGGTGATGTCAGAAGAAATGGCTCGAGCTCAGAAGATAAAAGA  
 TAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAAGATAACAATCAAATCCCAGATGCTGGT  
 CTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAGACCTACTTACAAAGTGGCATATA  
 TTGCAATTTATTTTAATTAAGATAACCTATTTATATATTTCTTTATAGAAAAAAGTCTGGAA  
 GAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTATAGGTGATTTTTCTTTTAATTC  
 TGTTAATTTATCTGTATTTCCCTAATTTTTCTACAATGAAGATGAATTCCTTGTATAAAATAA  
 GAAAAGAAATTAATCCTTGAGGTAAGCAGAGCAGACATCATCTCTGATTGTCCTCAGCCTCCAC  
 TTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGGTTGTAGTAGTGATCA  
 GGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCT  
 CTGGGTAAGGAACCTAAAGAACAAAAATCATCTGGTAATTCTTTCCTAGAAGGATCACAGCCC  
 CTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGAATTGTGTCC  
 CCTCAAATTCACATCCTTCTTGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTG  
 CAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCAATATGACTG  
 GTTTCCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTAAAG  
 ATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACCA  
 TCAGAAGCTTGGAAGAGGCAAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCT  
 GCTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAGAATAAATTTTCGGCTGTTT  
 TAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATC  
 CCTGTCTCCTCGTGTTTACATTCTGTGTGTGTCCCCTCCCACAATGTACCAAAGTTGTCTTTG  
 TGACCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACAC  
 TGCAGCTTCTACTTGAGCCCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACT  
 CGCTCTGGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAA  
 AATGAAGTCTCCTGCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATC  
 GATGTTTGTGTTTTAAGTTGCTCAGTTTTGGTCTAACTTGTTATGCAGCAATAGATAAATAA  
 TATGCAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESVVPNRWLDASLSPVILGVQG  
GSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPE  
ADQPVRLTQLPENG GWNAPITDFYFQQCD

### **N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

### **Interleukin-1 signature.**

amino acids 111-131

### **Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103



**FIGURE 153**

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCA**ATG**GCC  
GCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTC  
TTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAG  
TCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTG  
GCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGT  
GAGCGCTGCTATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTCCCTCAA  
TCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGG  
CTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAG  
GACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTG  
TTTATGTCTCTGAGAAATGCCTGCATT**TGA**CCAGAGCAAAGCTGAAAAATGAATAACTAACCC  
CCTTTCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAGGAAGA  
TGGAAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGG  
AAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTG  
ATAACATTTTCATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTTTTTAAATAATTGTC  
TTTTTCCATAAAAAAGATTACTTTCCATTCCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATG  
TTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAAGACTGCATTTTAT  
TTATATCATTTTATTAAATATGGATTTATTTATAGAAACATCATTCGATATTGCTACTTGAGTG  
TAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAACATGTTTATTTGACCTCAA  
TAAACACTTGGATATCCC

## **FIGURE 154**

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEA  
SLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLARLS  
NRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

#### **N-myristoylation sites.**

amino acids 14-20, 82-88

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

**FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCT  
GTCAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTCAGTGCAGA  
GGGCTGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGG  
CCAAGCTGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGG  
GTGCAGATGAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAG  
GTGGTTGCATTCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGC  
CCCAGCAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCC  
CTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTC  
AACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAG  
GACCTGTACCACGCCCCGTTGCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATG  
GACCCCCGGGGCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGC  
CATGGCGAGAAGGGCACCCACAAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTTCCTTA  
GCTTGTGTGTGTGTGCGGCCCCGTGTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTT  
TTGGGAAACCTGGAGCCAGGTGTACAACCACTTGCCATGAAGGGCCAGGATGCCCAGATGCTT  
GGCCCCTGTGAAGTGCTGTCTGGAGCAGCAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAA  
AACCTGCACTTCTGCACATTTTGAAAAGAGCAGCTGCTGCTTAGGGCCGCCGGAAGCTGGTGT  
CCTGTCATTTTCTCTCAGGAAAGGTTTTCAAAGTTCTGCCATTTCTGGAGGCCACCACTCCT  
GTCTCTTCCTCTTTTCCCATCCCCTGCTACCCTGGCCCAGCACAGGCACTTTCTAGATATTTT  
CCCCCTTGCTGGAGAAGAAAGAGCCCCTGGTTTTATTTGTTTGTGTTACTCATCACTCAGTGAGC  
ATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTTTTGACATGGATGATTCTGAGGAGGA  
AGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATATCTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPSKGQDTSEELLRWSTVPVPPLE  
PARPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDP  
RGNSELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-32

#### **N-glycosylation site.**

amino acids 136-140

#### **Tyrosine kinase phosphorylation site.**

amino acids 127-135

#### **N-myristoylation sites.**

amino acids 44-50, 150-156

**FIGURE 157**

CCGGCG**ATG**TCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG  
CCGACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA  
ATCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGAC  
TATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG  
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAAT  
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATC  
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGCAAT  
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA  
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT  
AAGAAGAATGAGGAGACAGTAGAAGTGAAC TTCACAACCACTCCCCTGGGAAACAGATACATG  
GCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA  
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTG  
ACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC  
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT  
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG  
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT  
CTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT  
CAAAACCATTGCAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG  
GGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCC  
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC  
TCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCAT  
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC  
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT  
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTG  
**TAG**

**FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPDGLRDLRVEPVTTTSVATGDYS  
 ILMNVSWVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF  
 PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK  
 NEETVEVNFTTTPLGNRYMALIQHSTIIIGFSQVFEPHQKKQTRASVVI PVTGDSEGATVQLTP  
 YFPTCGSDCIRHKGTVVLC PQTGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH  
 ERIKTSFSTTTLLPPIKVLVVPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKIAEMGP  
 VQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH  
 KYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQQVSAGKRSQACHDGCCSL

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201  
 and 283 - 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

**FIGURE 159**

AGCCACCAGCGCAAC**ATG**ACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTG  
CTGTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGA  
CATACTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGAC  
ATTGGCATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACC  
TCCCCCTGGAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCC  
CAGTGTAGGAACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTT  
CCCATCCAGCAAGAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAG  
TTGGAGAAGGTGCTGGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAG  
**TAA**GAGGTGCATATCCACTCAGCTGAAGAAG

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0  
1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0  
1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

## **FIGURE 160**

MTVKTLHGPA MVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIIN  
ENQRVSM SRNIESRSTSPWNYTVTWDPNRY PSEVVQAQCRNLGCINAQGKEDISMNSVPIQQE  
TLVVR RKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141



**FIGURE 161**

A C A C T G G C C A A A C A A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A  
 G G A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G G  
 A T T C C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T G G G G G G G G  
 C A G C A C A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G **A T G** C C T G T G C C C T G G T T C T T  
 G C T G T C C T T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A  
 G G A C G C T A C C C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A C A G T G A C A T A C T C T G C C T  
 G C C T G G G G A C A T C G T G C C T G C T C C G G G C C C C G T G C T G G C G C C T A C G C A C C T G C A G A C A G A G C T  
 G G T G C T G A G G T G C C A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G G C  
 C G T G C A T G G G C A C T G G G A A G A G C C T G A A G A T G A G G A A A G T T T G G A G G A G C A G C T G A C T C A G G  
 G G T G G A G G A G C C T A G G A A T G C C T C T C T C C A G G C C C A A G T C G T G C T C T C C T T C C A G G C C T A C C C  
 T A C T G C C C G C T G C G T C C T G C T G G A G G T G C A A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C  
 T G T G G G C T C T G T G G T A T A T G A C T G C T T C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C  
 C T A T A C T C A G C C C A G G T A C G A G A A G G A A C T C A A C C A C A C A G C A G C T G C C T G C C C T G C C C T G  
 G C T C A A C G T G T C A G C A G A T G G T G A C A A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A  
 C T T C G G C C T C T C C C T G T A C T G G A A T C A G G T C C A G G G C C C C C A A A A C C C C G G T G G C A C A A A A A  
 C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A C C A C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A  
 G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A C G A A C A T C T G C C C C T T C A G G G A G G A C C C C C G  
 C G C A C A C C A G A A C C T C T G G C A A G C C G C C C G A C T G C G A C T G C T G A C C C T G C A G A G C T G G C T G C T  
 G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T G T G C T G G C G G G C T C C G G G T G G G G A C C C  
 C T G C C A G C C A C T G G T C C C A C C G C T T T C C T G G G A G A A C G T C A C T G T G G A C A A G G T T C T C G A G T T  
 C C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G A A C A G C T C G G A G A A G C T G C A G C T  
 G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A G A C G A T G T G C T A C T G T T G G A G A C  
 A C G A G G C C C C C A G G A C A A C A G A T C C C T C T G T G C C T T G G A A C C C A G T G G C T G T A C T T C A C T A C C  
 C A G C A A A G C C T C C A C G A G G G C A G C T C G C C T T G G A G A G T A C T T A C T A C A A G A C C T G C A G T C A G G  
 C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G C C C C A T G G A C A A A T A  
 C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G C T G C G C T T T C C C T  
 C A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A C A G G A C G T C C G  
 C T C G G G G G C G G C C G C C A G G G G C C G C G C G G C T C T G C T C C C T A C T C A G C C G A T G A C T C G G G T T T  
 C G A G C G C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C G C T G C G C G T G G C C G T A G A  
 C C T G T G G A G C C G T C G T G A A C T G A G C G C G C A G G G G C C C G T G G C T T G G T T T C A C G C G C A G C G G C G  
 C C A G A C C C T G C A G G A G G G C G G C G T G G T G G T C T T G C T C T T C T C C C G G T G C G G T G G C G C T G T G  
 C A G C G A G T G G C T A C A G G A T G G G G T G T C C G G G C C C G G G G C G C A C G C C C G C A C G A C G C C T T C C G  
 C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C G C C C G G C A G C T A C G T G G G  
 G G C C T G C T T C G A C A G G C T G C T C C A C C C G G A C G C C G T A C C C G C C C T T T T C C G C A C C G T G C C C G T  
 C T T C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G C G  
 T T C C G G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G  
 C T A C T T C C A T C C C C C G G G G A C T C C C G C G C C G G G A C G C G G G G T G G G A C C A G G G G C G G G A C C T G G  
 G G C G G G G A C G G G A C T **T A A** A T A A A G G C A G A C G C T G T T T T T C T A A A A A A

**FIGURE 162**

MPVPWFLLSLALGRSPVVLSELRVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGPVLAP  
 THLQTELVLRQCQKETDCDLCLRVAVHLAVHGHWEPEDEEEKFGGAADSGVEEPRNASLQAQVV  
 LSFQAYPTARCVLLEVQVPAALVQFGQSVGQSVVYDCFEAALGSEVRIWSYTPRYEKELNHTQ  
 QLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPVKPRWHKNTGPKIITLNHTDL  
 VPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWLLDAPCSLPAEAALCW  
 RAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSEKLQLQECLWADSLGPLKD  
 DVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQSGQCLQLWDDDLGALW  
 ACPMDKYIHKRWALVWLACLLFAAALSLILLLKKDHAKGWLRLKQDVRSAAAARGRAALLLY  
 SADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFS  
 PGAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHPDAVPA  
 LFRTPVPVFTLPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGV  
 GPGAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
 334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
 692-697, 696-701, 700-705

**FIGURE 163**

GGGAGGGCTCTGTGCCAGCCCCG**ATG**AGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGG  
 CTGCTCACGCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACT  
 TTGAAAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCG  
 AGTATAAGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGGATCACCCGGA  
 AGTCTTGCAACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT  
 GTCAGTGCGGGAGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACT  
 ACCCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCAT  
 CCTACCCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTGGAAGACATCTTCCAT  
 GACCTGTTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAG  
 CAGAGAGAATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATT  
 TGGCTTCCACCTGGGCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGAC  
 CGGACATGGACCTACTCCTTCTCCGGAGCCTTCTGTTCTCCATGGGCTTCTCTGTCGAGTA  
 CTCTGCTACCTGAGCTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTC  
 CAGCGAGTCCTGACTTTCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTT  
 GACCTCAGCGGCCCCAGCAGTCTGGCCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGA  
 CCCAGGGAGCCCGCAGGAGCTCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAG  
 CCAGACATCTCCATCCTCCAGCCCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCC  
 TATGCCCCAAACGCTGCCCCTGAGGTGCGGCCCCCATCCTATGCACCTCAGGTGACCCCCGAA  
 GCTCAATTCCCATTCTACGCCCCACAGGCCATCTCTAAGGTCCAGCCTTCTCCTATGCCCCCT  
 CAAGCCACTCCGGACAGCTGGCCTCCCTCCTATGGGGTATGCATGGAAGGTTCTGGCAAAGAC  
 TCCCCCACTGGGACACTTTCTAGTCCTAAACACCTTAGGCCTAAAGGTGAGCTTCAGAAAGAG  
 CCACCAGCTGGAAGCTGCATGTTAGGTGGCCTTTCTCTGCAGGAGGTGACCTCCTTGGCTATG  
 GAGGAATCCCAAGAAGCAAAATCATTGCACCAGCCCCTGGGGATTTGCACAGACAGAACATCT  
 GACCCAAATGTGCTACACAGTGGGGAGGAAGGGACACCACAGTACCTAAAGGGCCAGCTCCCC  
 CTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTCCCTCCCTTTGCAACCTCCTTCCGGT  
 CCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCCTGCTGGAGTCCCTTGTGTGTCCC  
 AAGGATGAAGCCAAGAGCCCAGCCCCTGAGACCTCAGACCTGGAGCAGCCCACAGAACTGGAT  
 TCTCTTTTCAGAGGCCTGGCCCTGACTGTGCAGTGGGAGTCC**TGA**GGGGAATGGGAAAGGCTT  
 GGTGCTTCCCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCAATCCCATGCCTGCCCAT  
 GCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGCAGAGGGAGTGGCATG  
 CAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATAAGGACTGCAGCGG  
 GGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGCTCGCTGAGCCCTGCAAGGCAGAAA  
 TGACAGTGCAAGGAGGAAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTCCTAACACCA  
 TGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCTTGCCAGTTTCACAATCT  
 AGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTATTGTTCAAAGGTGGGAAGAGAGCCTG  
 GAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAACAACCTGCACT  
 TCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCAT  
 TCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTGAGCTTCATTCTCTGATAGAACAAAG  
 CGAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGAC  
 CCTATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCCCTGGACGGGTACAATAA  
 CACACTGTACTGATGTCACAACCTTTGCAAGCTCTGCCTTGGGTTGAGCCCATCTGGGCTCAAA  
 TTCCAGCCTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCGAGAACCTC  
 GGTTCCTCATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAA  
 ATGAAGTCATGTCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAAACGGT  
 AGCTATTTAAAAA

**FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTPVYSIEYKTYGER  
DWVAKKGCQRITRKSCNLTVETGNLTELYARVTAVSAGGRSATAKMTDRFSSLQHTTLKPPDV  
TCISKVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFF  
GLTPDTEFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYR  
YVTKPPAPPNSLVNQRVLTFQPLRFIQEHVLI PVFDLSGPSSLAQPVQYSQIRVSGPREPAGA  
PQRHSLSEITYLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPSPSYAPQVTPEAQFFFYA  
PQAISKVQPSSYAPQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPGQLQKEPPAGSCM  
LGGLSLQEVTS LAMEESQEAKSLHQPLGICTDRTS DPNVLHSGEEGTPQYLKGQLPLLSSVQI  
EGHPMSLPLQPPSGPCSPSDQGPSPWGLLESLVCPKDEAKSPAPETSDLEQPTELDSLFRGLA  
LTVQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

**FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAAC**AT**  
**G**GCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG  
 CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG  
 CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT  
 GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC  
 TTGGGCTGGAAGTGTGAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCA  
 TAAATACACGGAAGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG  
 AGGAAGAGATGATTTTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA  
 CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA  
 GGAGTCTCGGGGGCGTGAACCTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTCAGA  
 GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA  
 GAGCCACCTCAGACCAGCGTCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC  
 TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG  
 TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG  
 TCAGAGAGGAAGTGGACAGTGCCTTATTATTACAGCAAAGGATTTTCGTTGGCATCAAAATCT  
 AAGTTTGTTTTACAAAGATTGTTTT**TAG**TACTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCC  
 AAACAAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

165/168  
 TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAAC**AT**  
**G**GCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG  
 CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG  
 CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT  
 GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC  
 TTGGGCTGGAAGTGTGAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCA  
 TAAATACACGGAAGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG  
 AGGAAGAGATGATTTTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA  
 CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA  
 GGAGTCTCGGGGGCGTGAACCTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTCAGA  
 GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA  
 GAGCCACCTCAGACCAGCGTCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC  
 TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG  
 TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG  
 TCAGAGAGGAAGTGGACAGTGCCTTATTATTACAGCAAAGGATTTTCGTTGGCATCAAAATCT  
 AAGTTTGTTTTACAAAGATTGTTTT**TAG**TACTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCC  
 AAACAAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFVLGALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD CRF  
VNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKD LIKVLH KYTEEELHIPADETDFVC FE  
GGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRADS  
EDGEGAFSESTEGLOGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLKVP GSE SRTGN  
SSPASVEREKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

**FIGURE 167**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGGAAGAGAAGCAAAGC  
 GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAA  
 CTTCACTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGG  
 CACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGG  
 GCTCGGGCGGCGGGAGTAGGGCCCGGCAGGGAGGAGGAGGCTGCATATTCAGAGTTCGCGGG  
 CTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGA  
**TG**AGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCC  
 GCCGCGTGGTCAAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGG  
 CCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTG  
 AGGGAGGAGTCCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGC  
 AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGA  
 ATGGAGATGGGCAAACATCTGGTGCCTGCCAGATCTCTACCAGTGGTCTGATGGAAGCAATT  
 CCCAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAGTGTGTTGTGATGT  
 ATCACCACCAACTGCCAATCCTGGCCTTGGGGTCCCTACCTTTACCAGTGGAAATGATGACA  
 GGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTAATCCAACAGCCCCTG  
 TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAATGTGGTTGTTACTGAAG  
 CAGGTATAATTCCCAATCTAATTTATGTTGTTTATACCAACAATACCCCTGCTCTTACTGATAC  
 TGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTAAAGGAAGAACAAAACTA  
 GTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAGTAT  
**AA**TAACTCATTGACTTGGTTCCAGAATTTTGTAATTCTGGATCTGTATAAGGAATGGCATCAG  
 AACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAAGATGAACTGTAAGCTCCCCCT  
 TGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTTCAATTTAAAGAATATGCTGTGCTA  
 ATAATGGAGTGAGACATGCTTATTTTGTCTAAAGGATGCACCCAACTTCAAACCTCAAGCAAA  
 TGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT  
 TCCTTTTATTTCTTTACCTTTTATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATTGA  
 AATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGATAAAAATGAACTGTTCTA  
 ATATTTATTTTTATGGCATCTCATTTTTTCAATACATGCTCTTTTGATTAAAGAACTTATTAC  
 TGTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGTCTCTCGAA  
 ATAATTCATCTTTTACGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA  
 AGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATTGTCT  
 AATTTCAATTGTGCAAGACATGTGCCCTTATAATTATTTTTAGCTTAAAATTAAACAGATTTTG  
 TAATAATGTAACCTTGTGTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAGT  
 GACATACACAATATAAATCATATGTCTTACACGTTGCCTATATAATGAGAAGCAGCTCTCTG  
 AGGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTT  
 GGGATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGC  
 CTCTGACTATATTAGTATACAAAGAGGTGATGTGGTTGAGACCAGGTGAATAGTCACTATCAG  
 TGTGGAGACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAA  
 ATGGGTTGGAACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATG  
 GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGA  
 AAGTTGTAACCTCTCTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTG  
 TTTCTGGGGGAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFRRVVSQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACES  
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDWIGLWRNGDGQTSACPDLYQWSDGSN  
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP  
VEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKT  
SPNQSTLWISKSTRKESGMEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 214-235

#### **N-glycosylation sites.**

amino acids 86-89, 255-258

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

#### **N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217